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(54) Title: NUCLEIC ACIDS, PROTEINS, AND ANTIBODIES

(57) Abstract: The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Nucleic Acids, Proteins, and Antibodies

[1] This application refers to a "Sequence Listing" that is provided only on electronic media in computer readable form pursuant to Administrative Instructions Section 801(a)(i). The Sequence Listing forms a part of this description pursuant to Rule 5.2 and Administrative Instructions Sections 801 to 806, and is hereby incorporated in its entirety.

[2] The Sequence Listing is provided as an electronic file (PTZ15PCT_seqList.txt, 1,891,228 bytes in size, created on January 13, 2001) on four identical compact discs (CD-R), labeled "COPY 1," "COPY 2," "COPY 3," and "CRF." The Sequence Listing complies with Annex C of the Administrative Instructions, and may be viewed, for example, on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, version 2000 (see World Wide Web URL: http://www.fileviewer.com).

Field of the Invention

[3] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic

methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

[4] The Human genome is estimated to contain roughly 100,000 genes, each of which plays an important function in sustaining life. Each of these roughly 100,000 genes encodes for a corresponding protein which can be classified based upon its structure and/or function. Some proteins are secreted, while other proteins reside either as membrane associated proteins or intracellularly. Although protein sequences vary substantially, many patterns and overall properties are shared, such as, for example, amino-terminal signal sequences.

[5] Some proteins, for example secreted proteins, contain an amino-terminal signal sequence which facilitates protein transport. This amino-terminal signal sequence directs, or targets, the protein from its ribosomal assembly site to a particular cellular or extracellular location. Transport may involve any combination of several of the following steps: contact with a chaperone, unfolding, interaction with a receptor and/or a pore complex, addition of energy, and refolding. Moreover, an extracellular protein may be produced as an inactive precursor. Once the precursor has been exported, removal of the signal sequence by a signal peptidase activates the protein. Examples of some protein families that contain signal sequences include cytokines (chemokines) and hormones (growth and differentiation factors). Computer algorithms can be generated to identify amino-terminal signal sequences. Examples of computer programs designed to identify amino-terminal signal sequences include hidden Markov models (HMMs), statistical alternatives to FASTA and Smith Waterman algorithms, which have been used to find shared patterns, specifically consensus sequences (Pearson, W.R., and D.J. Lipman, *PNAS*, 85:2444-48 (1988); Smith, T.F., and M.S. Waterman, *J. Mol. Biol.*, 147:195-97 (1981)). These algorithms are quite flexible in that they incorporate information from newly identified sequences to build even more successful patterns.

[6] Other families of proteins exist as membrane associated proteins. Examples of some of these membrane associated protein families include receptors (nuclear, 4

transmembrane, G protein coupled, and tyrosine kinase), protein kinases, phosphatases, neuropeptides and vasomediators, G proteins, ion channels (calcium, chloride, potassium, and sodium), proteases, transporter/pumps (amino acid, sugar, protein, metal and vitamin; calcium, phosphate, potassium, and sodium), matrix molecules (adhesion, cadherin, extracellular matrix molecules, integrin, and selectin), and regulatory proteins. Again, computer programs can aid in the discovery of these molecules. For example, Klein et al. have developed a method ("ALOM", also called as KKD) to detect potential transmembrane segments in polypeptides (Klein, P., et al., Biochim. Piophys. Acta., 815:468 (1985)). It attempts to identify the most probable transmembrane segment from the average hydrophobicity value over a range of amino acid residues. It predicts whether the segment is a transmembrane segment (INTEGRAL) or not (PERIPHERAL), and thus can suggest membrane association of a polypeptide.

[7] Furthermore, some proteins function intracellularly, and can be identified by their structure and/or function. Computer algorithms can be adapted to aid in the identification of novel members of intracellular protein families. Examples of intracellular proteins include transcription factors, various classes of enzymes, Mitochondrial proteins, and signal transduction molecules.

[8] Descriptions of some of these proteins (e.g., receptors, hormones, and matrix proteins) and diseases associated with their dysfunction follow.

Summary of the Invention

[9] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[10] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which

the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ^{33}P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[11] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[12] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise,

or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[13] Table 3 provides polynucleotide sequences that may be disclaimed according to certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[14] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[15] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.

[16] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[17] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

[18] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

[19] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[20] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

[21] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence

contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[22] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore,

it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[23] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[24] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[25] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions

include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[26] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[27] Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[28] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[29] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be

modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[30] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1Aor 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.

[31] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity,

antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

[32] The polypeptides of the invention can be assayed for functional activity (e.g. biological activity) using or routinely modifying assays known in the art, as well as assays described herein. Specifically, one of skill in the art may routinely assay human polypeptides (including fragments and variants) of the invention for activity using assays as described in the examples section below.

[33] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[34] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the Invention

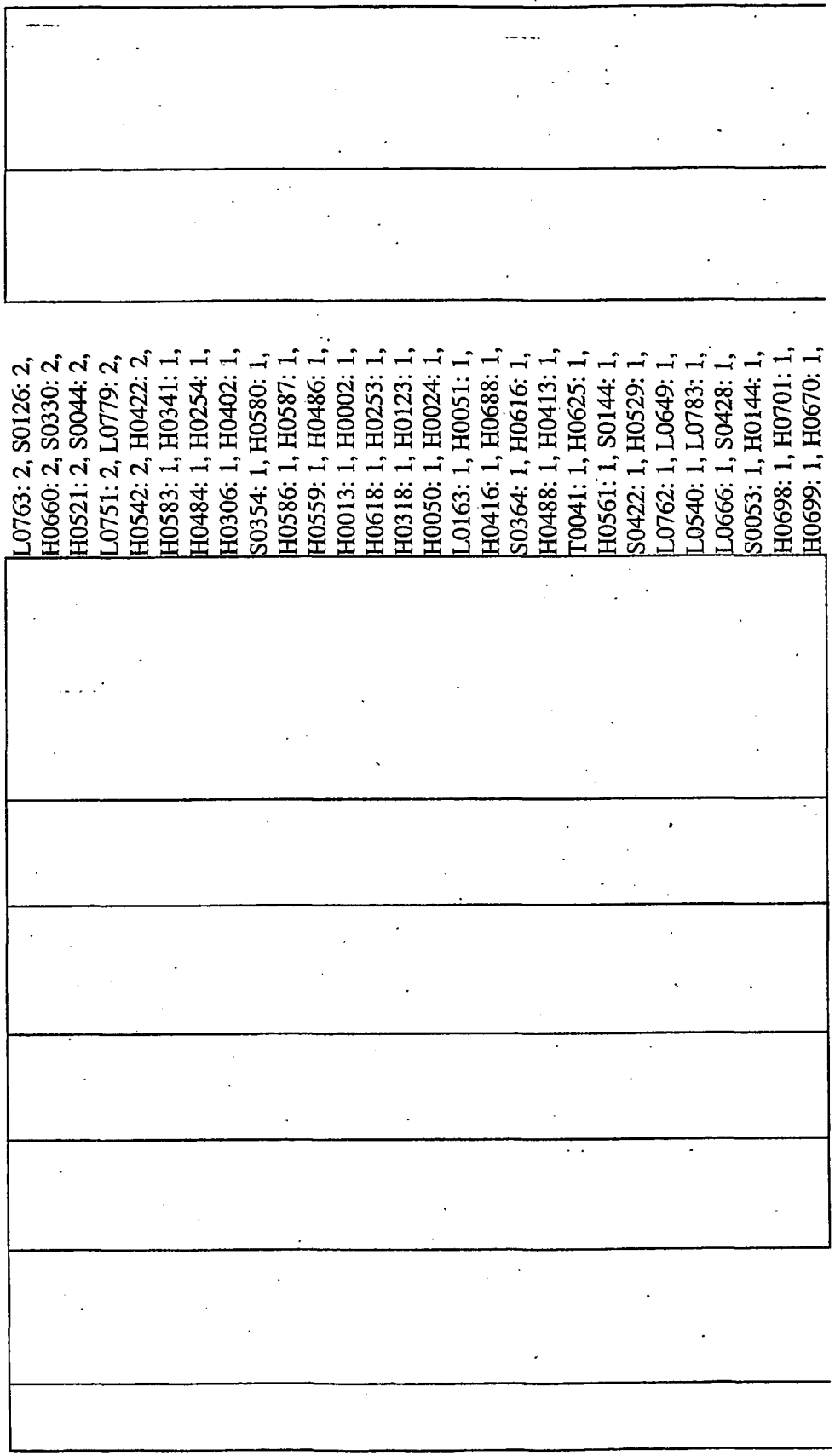
TABLE 1A

Gene No:	Clone ID NO: Z	Contig ID:	SEQ ID NO: X	ORF (From-To)	AA SEQ ID NO: Y	Predicted Epitopes	Tissue Distribution Library code: count (see Table IV for Library Codes)	Cytologic Band	OMIM Disease Reference(s):
1	HFRBN59	1106393	11	1 - 243	335	Pro-1 to Arg-6, Gln-38 to Ser-44.	AR089: 2, AR061: 1 S0050: 1 and S0260: 1.		
		739539	237	77 - 232	561	Gln-9 to Ser-15.			
2	HE2KJ64	906019	12	2 - 778	336	His-1 to Phe-10, Asp-17 to Phe-22, Pro-25 to Phe-36, Tyr-84 to Trp-90, Pro-95 to Ser-103, Cys-118 to Thr-134.	AR089: 1, AR061: 1 L0362: 3, L0794: 2, H0624: 1, L0471: 1, H0622: 1, H0539: 1, L0439: 1 and L0581: 1.		
3	HAGDV32	1178626	13	247 - 516	337	Pro-1 to Ile-13, Gly-51 to Gln-56, Arg-63 to Thr-68, Ser-75 to Phe-81.	AR061: 3, AR089: 3 L0758: 2, S0010: 1, L0471: 1 and L0439: 1.		
		699372	238	2 - 250	562				
4	HLICC37	856958	14	2 - 346	338	Ala-47 to Ser-62, Glu-70 to Pro-76.	AR061: 13, AR089: 10 L0769: 4, L0717: 3,		

5	HBGBU96	1121900	15	3 - 449	339	Ala-61 to Ala-68.	L0766: 3, L0774: 3, L0775: 3, H0529: 2, L0747: 2, L0756: 2, L0777: 2, H0650: 1, H0663: 1, S0442: 1, S0358: 1, S0278: 1, H0549: 1, H0318: 1, H0052: 1, L0738: 1, H0620: 1, H0014: 1, H0355: 1, H0213: 1, H0606: 1, S0448: 1, S0142: 1, L0770: 1, L0646: 1, L0773: 1, L0651: 1, L0659: 1, L0518: 1, L0663: 1, H0547: 1, H0659: 1, H0539: 1, L0748: 1, L0750: 1, S0260: 1 and H0422: 1.	AR089: 1, AR061: 1 H0617: 2, S0031: 2, S0132: 1 and H0181: 1.		
		848220	239	3 - 653	563	Ala-61 to Ala-68.				
6	HAJCQ63	823850	16	1 - 579	340	Pro-101 to Arg-106, Lys-140 to His-145, Pro-158 to Val-163.	AR089: 1, AR061: 1 L0766: 4, H0038: 1, H0616: 1, H0561: 1, L0763: 1, H0521: 1, L0750: 1, L0780: 1,			

							L0758: 1 and L0595: 1.		
7	HLMMV66	1153903	17	621 - 166	341	Arg-14 to Arg-22, Pro-62 to Ala-79, Phe-106 to Arg-114, Glu-120 to Gly-125.	AR061: 7, AR089: 5 H0255: 2, L0493: 2 and L0662: 1.		
		926188	240	218 - 448	564				
8	HLWAR08	1096389	18	1 - 531	342	Tyr-47 to His-53, Lys-87 to Tyr-95, Ser-110 to Ser-116, Thr-124 to Ala-129, Trp-146 to Arg-152.	AR089: 4, AR061: 2 L0539: 1 and H0553: 1.		
		959139	241	3 - 290	565	Tyr-46 to His-52.			
9	HBGTT76	1152327	19	1 - 468	343	Pro-64 to Gly-71, Lys-101 to Trp-106, Glu-108 to Gly-116.	AR089: 46, AR061: 9 H0617: 1		
		903653	242	14 - 556	566	His-8 to Gly-18, Pro-89 to Gly-96, Lys-126 to Trp-131, Glu-133 to Gly-141.			
10	HMCFO24	924647	20	3 - 500	344	Val-30 to Leu-35, Asn-65 to Leu-71, Val-144 to Phe-149.	AR061: 3, AR089: 1 H0457: 5, L0766: 5, H0581: 2, H0090: 2, H0521: 2, L0748: 2, H0171: 1, H0656: 1, S0212: 1, S0140: 1, H0486: 1, H0156: 1, L0471: 1, T0041: 1,		

							S0344: 1, S0426: 1, L0387: 1, L0776: 1, L0655: 1, L0367: 1, L0792: 1, L0438: 1, H0690: 1, H0539: 1, H0436: 1, L0439: 1, L0779: 1, L0780: 1, L0755: 1 and H0422: 1.		
11	HBIOM94	973137	21	449 - 760	345	Trp-1 to Asp-13.	AR089: 10, AR061: 4 L0759: 2 and H0593: 1.		
12	HBJLR11	1012465	22	397 - 2	346		AR089: 8, AR061: 5 H0677: 54, L0604: 11, S0366: 7, L0766: 6, H0445: 6, H0543: 6, H0556: 5, H0650: 5, H0255: 5, L0770: 5, L0655: 5, H0436: 5, L0777: 5, L0485: 5, H0657: 4, H0581: 4, L0769: 4, L0761: 4, L0747: 4, H0656: 3, H0599: 3, H0196: 3, H0373: 3, H0271: 3, L0520: 3, L0546: 3, H0423: 3, H0305: 2, H0333: 2, L0623: 2, H0457: 2, H0100: 2,		


L0763: 2, S0126: 2,
H0660: 2, S0330: 2,
H0521: 2, S0044: 2,
L0751: 2, L0779: 2,
H0542: 2, H0422: 2,
H0583: 1, H0341: 1,
H0484: 1, H0254: 1,
H0306: 1, H0402: 1,
S0354: 1, H0580: 1,
H0586: 1, H0587: 1,
H0559: 1, H0486: 1,
H0013: 1, H0002: 1,
H0618: 1, H0253: 1,
H0318: 1, H0123: 1,
H0050: 1, H0024: 1,
L0163: 1, H0051: 1,
H0416: 1, H0688: 1,
S0364: 1, H0616: 1,
H0488: 1, H0413: 1,
T0041: 1, H0625: 1,
H0561: 1, S0144: 1,
S0422: 1, H0529: 1,
L0762: 1, L0649: 1,
L0540: 1, L0783: 1,
L0666: 1, S0428: 1,
S0053: 1, H0144: 1,
H0698: 1, H0701: 1,
H0699: 1, H0670: 1,

							H0518: 1, H0522: 1, L0741: 1, L0750: 1, L0752: 1, L0731: 1, L0757: 1 and L0584: 1.		
		956568	243	2118 - 478	567	Asp-27 to His-32, Gln-65 to Gly-76, Lys-80 to Ser-94, Pro-99 to Asn-104, Gly-126 to Lys-143, Pro-150 to Lys-156, Glu-163 to Glu-175, Val-193 to Asp-204, Met-230 to Ser-263, Ala-278 to Gly-291, Pro-306 to Asn-320, Asn-328 to Lys-333, Glu-348 to Glu-355, Ile-358 to Asn-363, Glu-375 to Ser-381, Lys-390 to Arg-395, Lys-433 to Asn-441, Ser-456 to Phe-463, Glu-484 to Lys-490, Glu-498 to Gly-507, Glu-535 to Glu-547.			
		975276	244	1024 - 632	568	Arg-1 to Ala-7, Thr-75 to Pro-94, Arg-111 to Gly-118,			

13	HLTER04	590990	23	3 - 938	347	Asp-122 to Gln-130.	His-1 to Glu-14, Asp-26 to Lys-34, Ser-47 to Lys-52, Asn-97 to Gly-107, Lys-123 to Gln-129, Glu-215 to Asp-228, Pro-245 to Glu-250, Leu-255 to Glu-260, Glu-275 to Gly-306.	AR089: 25, AR061: 15 L0565: 6, H0090: 4, L0439: 4, L0779: 4, L0666: 3, S0360: 2, S0051: 2, H0553: 2, L0766: 2, L0438: 2, S0126: 2, H0521: 2, L0740: 2, L0747: 2, L0749: 2, L0731: 2, L0758: 2, S0192: 2, H0583: 1, S0212: 1, S0442: 1, S0132: 1, H0441: 1, H0431: 1, H0586: 1, H0497: 1, H0069: 1, H0075: 1, S0346: 1, S0474: 1, H0046: 1, H0355: 1, H0267: 1, S0003: 1, H0328: 1, H0615: 1, H0428: 1, T0006: 1, H0163: 1, H0038: 1, H0040: 1, H0623: 1, H0560: 1, H0633: 1, S0344: 1, S0002: 1, S0426: 1, L0770: 1, L0772: 1, L0764: 1, L0776: 1, L0655: 1,		

							L0659: 1, L0783: 1, L0789: 1, H0144: 1, H0520: 1, H0683: 1, H0670: 1, H0660: 1, S0328: 1, L0748: 1, L0780: 1, L0757: 1, L0599: 1, S0026: 1 and H0543: 1.		
14	HMSMU30	1050601	24	2 - 310	348	Asn-58 to Gly-64.	AR089: 11, AR061: 9 H0050: 2, H0494: 1 and S0426: 1.		
		823859	245	2 - 310	569	Asn-58 to Gly-64.			
15	H2MBY83	752124	25	2 - 493	349	Glu-1 to Lys-27, Thr-77 to Leu-82, Asp-114 to Lys-119, Ser-130 to Thr-138.	AR089: 34, AR061: 16 T0109: 1 and S0310: 1.		
16	HBUAH93	1164739	26	1 - 1344	350	Gly-1 to Glu-12, Glu-22 to Gly-35, Pro-37 to Thr-49, Tyr-72 to Asn-81, Arg-191 to Asp-196, Gly-211 to Thr-218, Ala-256 to Asn-261, Gln-269 to Phe-282, Leu-286 to Arg-293, Phe-393 to Asp-400, Thr-407 to Thr-414.	AR061: 3, AR089: 1 H0547: 2, H0583: 1, S0182: 1, H0327: 1, L0471: 1, H0264: 1, H0539: 1, S0152: 1, H0521: 1 and H0343: 1.		
		810424	246	1 - 489	570	Gly-1 to Glu-12,			

17	HMZAD58	975304	27	293 - 2509	351	Glu-22 to Gly-35, Pro-37 to Thr-49. Ser-40 to Ser-45, His-75 to Trp-81, Ser-113 to Lys-128, Pro-146 to Thr-154, Asp-217 to Val-229, Gly-261 to Gln-270, Glu-313 to Thr-319, Pro-346 to Leu-359, Ala-378 to Ser-385, Ser-388 to Asn-393, Val-407 to Asp-418, Ser-422 to Leu-428, Thr-431 to Leu-441, Leu-478 to Ala-489, Gly-499 to Pro-522, Glu-527 to Tyr-535, Glu-540 to Arg-550, Arg-560 to Arg-593, Arg-625 to Ile-630, Gln-642 to Tyr-649, Lys-669 to Met-675, Ala-687 to Thr-706, Thr-734 to Asn-739.	AR089: 3, AR061: 2 L0749: 7, S0002: 5, L0766: 4, L0771: 3, L0740: 3, H0657: 2, H0266: 2, H0598: 2, H0623: 2, H0521: 2, L0755: 2, S0342: 1, T0049: 1, S0132: 1, H0261: 1, H0438: 1, H0333: 1, H0486: 1, H0013: 1, H0156: 1, H0050: 1, H0591: 1, H0264: 1, L0564: 1, H0560: 1, H0561: 1, L0773: 1, L0521: 1, L0768: 1, L0803: 1, L0774: 1, L0665: 1, H0648: 1, S0032: 1, L0748: 1, L0439: 1, L0747: 1, L0758: 1, S0260: 1, H0665: 1 and H0542: 1.			
18	HCHNH17	975378	28	2 - 1021	352	Pro-78 to Lys-86, Cys-88 to Leu-97, Asp-100 to Ile-107,	AR061: 1, AR089: 0 H0599: 25, L0731: 19, L0750: 14, L0754: 13,	3q13.3-q21	106165, 117700, 117700,	

							126451, 150210, 169600, 180380, 180380, 180380, 190000, 203500, 232050, 276902, 60882, 601199, 601199, 601199, 601471, 601682
						L0766: 8, L0776: 8, L0752: 8, L0757: 8, L0747: 6, L0744: 5, L0769: 4, L0779: 4, L0777: 4, S0420: 3, L0770: 3, L0755: 3, L0758: 3, L0471: 2, L0771: 2, L0775: 2, L0806: 2, L0659: 2, S0126: 2, H0670: 2, L0743: 2, L0759: 2, L0604: 2, H0624: 1, H0685: 1, H0650: 1, H0484: 1, H0483: 1, H0661: 1, S0358: 1, S0360: 1, S0046: 1, H0411: 1, H0632: 1, H0427: 1, S0280: 1, H0097: 1, H0004: 1, S0049: 1, H0028: 1, H0622: 1, L0142: 1, H0591: 1, L0763: 1, L0772: 1, L0800: 1, L0764: 1, L0662: 1, L0768: 1, L0794: 1, L0774: 1, L0807: 1, L0809: 1, L0666: 1, L0665: 1, S0148: 1,
					Pro-176 to Pro-181, Arg-191 to Met-196, Pro-200 to Arg-210, Pro-246 to Ala-259, Ser-271 to Glu-276, Asp-298 to Trp-306, Pro-332 to Ser-340.		

									S0328: 1, S0406: 1, S3014: 1, S0027: 1, S0028: 1, L0599: 1, S0026: 1 and H0667: 1.		
19	HBWAJ55	802098	29	2 - 64	353	Asn-7 to Asn-12.			AR089: 0, AR061: 0 S0021: 1		
		971772	247	22 - 1299	571	Glu-19 to Asn-42, Ala-135 to Gly-140.					
20	HNJCE31	1152346	30	1266 - 244	354	Ser-21 to Leu-26, Leu-63 to Ser-76, Ala-141 to Pro-153, Pro-184 to Leu-194, Gln-235 to Gly-240, Pro-279 to Asp-288, Lys-296 to Pro-302.			AR061: 1, AR089: 1 L0771: 3, L0766: 3, L0779: 3, H0485: 2, H0424: 2, L0769: 2, L0758: 2, H0657: 1, H0656: 1, H0635: 1, H0634: 1, H0059: 1, S0386: 1, L0763: 1, L0761: 1, L0644: 1, L0768: 1, L0803: 1, S0328: 1, H0539: 1, H0521: 1, H0522: 1, S3012: 1, L0751: 1, L0745: 1, L0752: 1, L0755: 1, L0581: 1 and S0026: 1.		
		911597	248	3 - 1031	572	Gly-9 to Gly-18, Arg-23 to Leu-28, Leu-65 to Ser-78, Ala-143 to Pro-155,					

21	HKAIU14	919538	31	1 - 1347	355	Pro-186 to Leu-196, Gln-237 to Gly-242, Pro-281 to Asp-290, Lys-298 to Pro-304.	Glu-14 to Ala-21, Lys-51 to Ser-59, Ile-70 to Phe-75, Ala-107 to Arg-113, Thr-124 to Asn-131, Tyr-171 to Asn-176, Gln-187 to Asn-238, Ser-243 to Ile-248, Glu-265 to Ser-271, Pro-281 to Glu-298, Ser-309 to Met-316, Pro-321 to Pro-329, Gln-374 to Arg-381, Asp-390 to Cys-400.	AR089: 9, AR061: 4 L0766: 7, L0759: 4, L0757: 3, S0354: 2, H0251: 2, L0783: 2, L0439: 2, L0605: 2, H0650: 1, H0657: 1, H0664: 1, S0376: 1, S0360: 1, H0421: 1, H0510: 1, S0250: 1, H0622: 1, H0033: 1, H0169: 1, H0616: 1, H0551: 1, H0494: 1, H0641: 1, L0763: 1, L0772: 1, L0655: 1, S0052: 1, L0438: 1, H0660: 1, S0330: 1, H0521: 1, L0599: 1 and H0542: 1.		
22	HCE4I12	911586	32	1 - 315	356			AR061: 5, AR089: 2 S0222: 5, S0007: 2, H0013: 2, L0471: 2, H0622: 2, H0264: 2, L0803: 2, L0438: 2, L0745: 2, H0542: 2,		

23	HFOYI18	926488	33	12 - 986	357		H0624: 1, H0556: 1, H0411: 1, T0082: 1, S0010: 1, H0052: 1, L2250: 1, H0009: 1, T0010: 1, S6028: 1, S0038: 1, L0641: 1, L0643: 1, L0374: 1, L0662: 1, L0794: 1, L0766: 1, L0804: 1, L0523: 1, L0805: 1, L0655: 1, L0606: 1, L0791: 1, H0547: 1, H0519: 1 and H0689: 1.		
24	HHEDM89	945055	34	1 - 903	358	Glu-1 to Phe-7, Pro-9 to Asn-14,	AR089: 1, AR061: 0 L0794: 3, H0265: 1, T0002: 1, S0116: 1, S0360: 1, H0486: 1, H0581: 1, H0052: 1, H0615: 1, S0036: 1, H0623: 1, L0766: 1, L0803: 1, L0659: 1, L0783: 1, S3014: 1, L0747: 1, L0749: 1, L0777: 1, L0595: 1, H0667: 1, S0276: 1 and H0543: 1.	AR089: 2, AR061: 1 L0779: 5, L0157: 2,	

					Ser-86 to Ser-92.	L0803: 2, L0754: 2, L0595: 2, H0305: 1, H0589: 1, H0638: 1, H0351: 1, H0486: 1, S0280: 1, L0021: 1, H0318: 1, H0596: 1, S0150: 1, S0144: 1, L0364: 1, L0766: 1, L0809: 1, L0532: 1, H0667: 1 and H0542: 1.		
25	HFXKW18	945288	35	421 - 2337	359	Val-12 to Gln-17, Ala-75 to Arg-82, Lys-112 to Ile-117, Asn-179 to Trp-185, Asp-190 to Lys-209.	AR061: 2, AR089: 1 H0250: 3, S0031: 3, H0271: 2, S0260: 2, S0001: 1, S0282: 1, H0617: 1, L0367: 1, S0053: 1, S0390: 1, L0698: 1 and H0352: 1.		
26	HBIMF04	951601	36	3 - 1229	360		AR089: 3, AR061: 2 L0766: 8, H0457: 7, H0436: 5, L0747: 4, H0486: 3, H0620: 3, H0520: 3, H0341: 2, H0255: 2, H0402: 2, S0358: 2, H0618: 2, H0581: 2, H0024: 2, H0405: 2, H0617: 2, L0761: 2, L0662: 2, L0768: 2, L0803: 2,		

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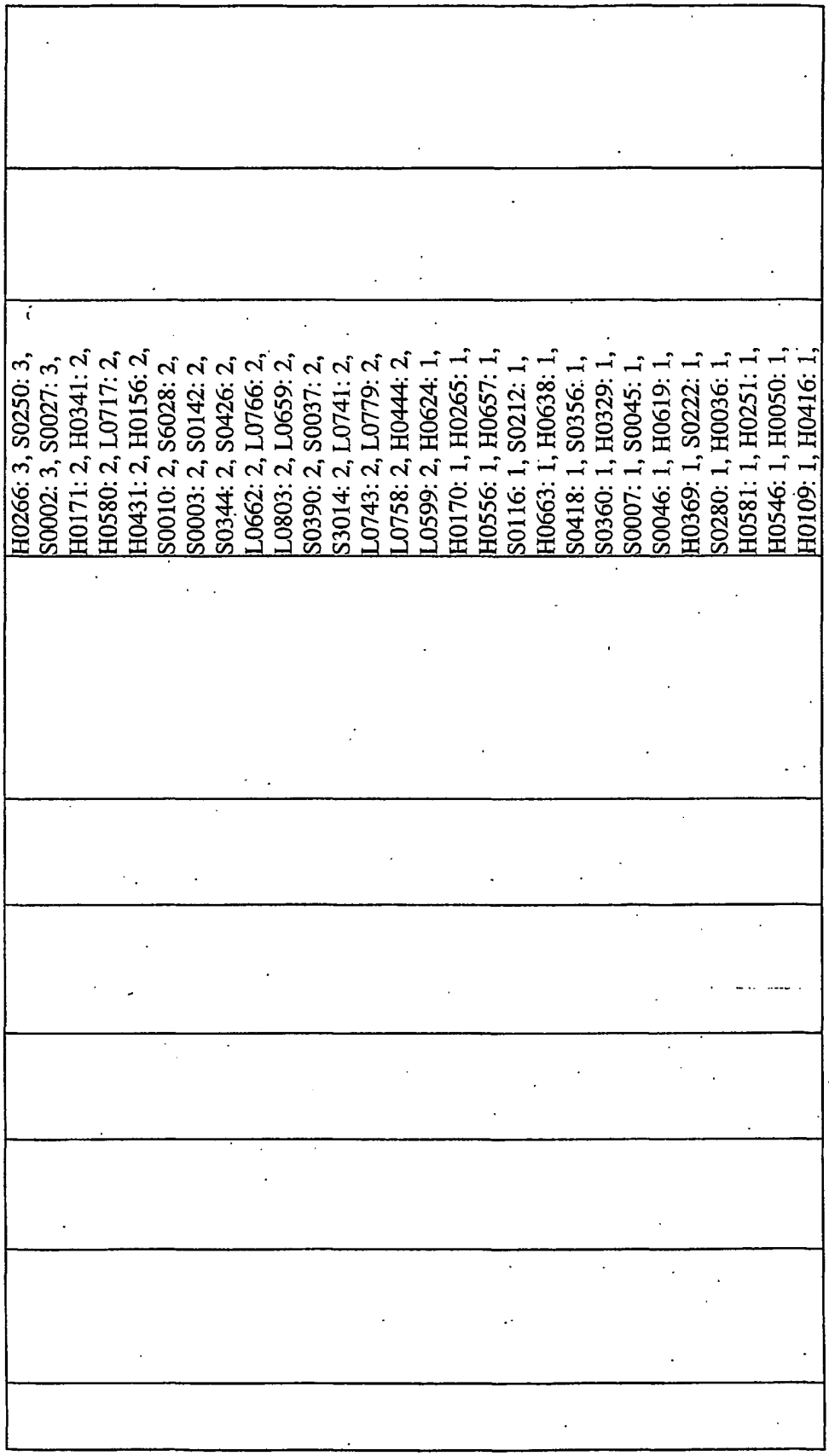
27	HEEAU28	912280	37	610 - 449	361	Leu-10 to Pro-28.		AR061: 6, AR089: 3 L0751: 3, L0747: 2, L0361: 2, H0549: 1, H0550: 1, S0280: 1, H0009: 1, H0123: 1, H0620: 1, H0594: 1, H0688: 1, L0800: 1, L0662: 1, L0766: 1, L0803: 1, L0791: 1, L0666: 1, L0663: 1, L0665: 1, H0689: 1, S0390: 1, L0439: 1, L0777: 1 and L0731: 1.		
		946972	249	1 - 441	573	Arg-7 to Tyr-12, Ser-46 to Lys-54, Gln-138 to Ile-147.				
28	HDPKI66	823854	38	2 - 1378	362	Arg-13 to Ser-20, Asn-88 to Lys-94, Met-108 to Glu-113, Ala-154 to Phe-159, Arg-172 to Cys-202.		AR089: 2, AR061: 0 L0748: 11, L0749: 10, L0777: 10, H0521: 9, H0144: 8, L0740: 7, H0013: 5, H0620: 5, H0069: 4, L0754: 4,		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29	HOCQD08	972981	39	2 - 715	363	Ile-46 to Arg-53, Phe-78 to Pro-86, Leu-112 to Val-119, Ile-125 to Thr-130, Pro-140 to Gly-152, Arg-187 to Glu-199.	AR089: 3, AR061: 2 H0556: 10, L0748: 8, H0620: 7, L0747: 7, L0637: 5, H0265: 4, H0013: 4, H0551: 4, L0776: 4, L0663: 4,	S0214: 1, H0428: 1, H0622: 1, H0031: 1, H0111: 1, H0165: 1, L0455: 1, H0090: 1, H0634: 1, H0616: 1, H0551: 1, L0564: 1, H0641: 1, H0646: 1, S0144: 1, S0422: 1, H0695: 1, L0521: 1, L0767: 1, L0804: 1, L0658: 1, L0656: 1, L0790: 1, L0791: 1, L0792: 1, L0438: 1, S0126: 1, H0435: 1, H0648: 1, H0539: 1, H0522: 1, H0631: 1, S0028: 1, L0747: 1, L0731: 1, L0759: 1, L0583: 1, S0011: 1, H0136: 1, S0192: 1, S0276: 1, H0543: 1, H0423: 1 and L0600: 1.

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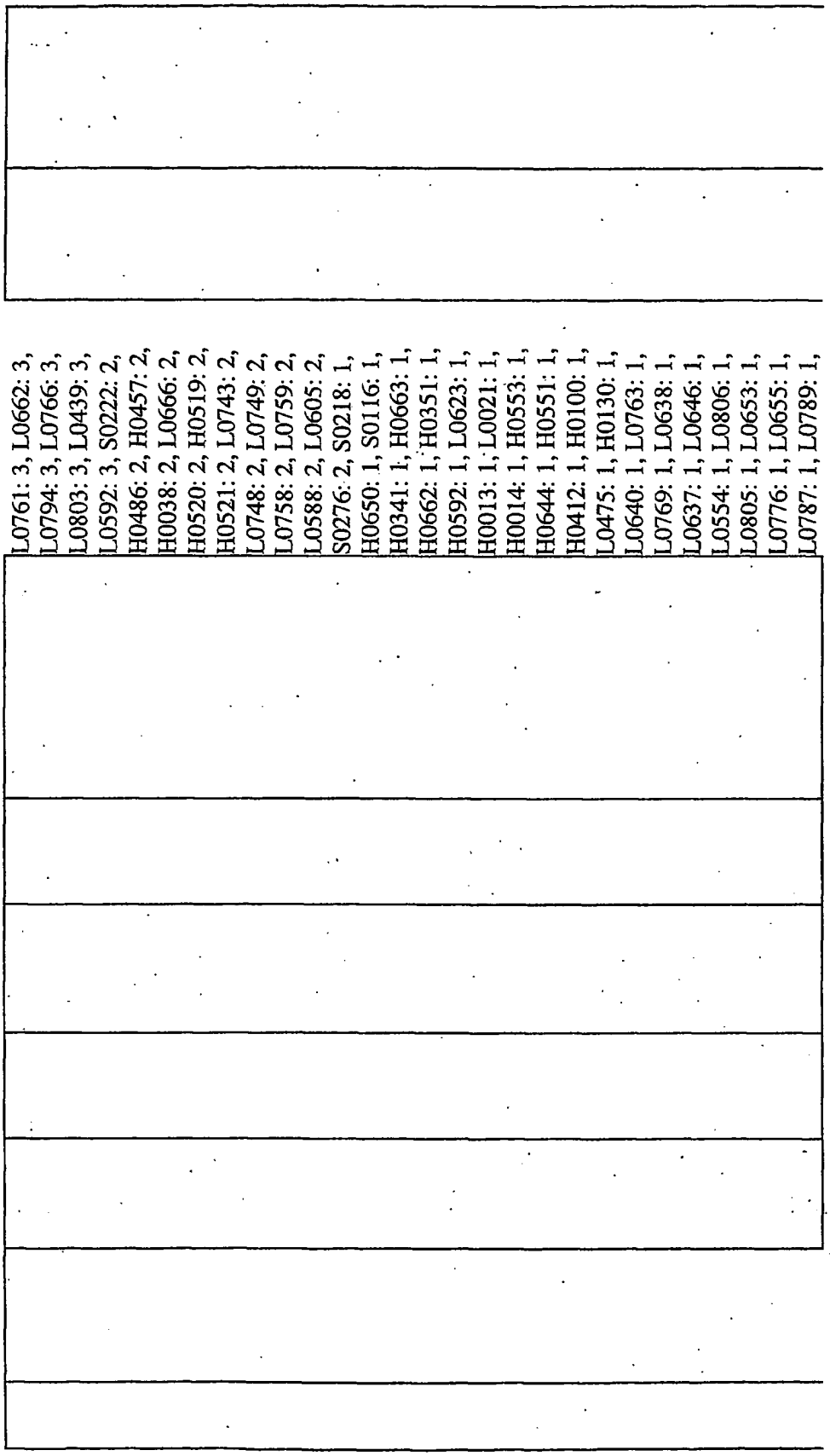
30	HDPRP54	1228283	40	48 - 1940	364	Gln-18 to Gly-32, Val-84 to Asn-91, Ala-286 to Leu-292, Lys-412 to Lys-419, Arg-460 to Cys-465, Phe-510 to Leu-515, Leu-567 to Gln-576.	L0759: 1, L0588: 1, L0362: 1, L0361: 1, H0653: 1, H0136: 1, S0196: 1, H0543: 1 and S0424: 1.	AR089: 3, AR061: 1 H0486: 3, S0422: 3, L0665: 3, L0527: 2, L0758: 2, L0596: 2, S0358: 1, S0360: 1, S0132: 1, H0586: 1, H0497: 1, H0318: 1, H0046: 1, S0051: 1, H0615: 1, H0032: 1, H0673: 1, S0036: 1, H0038: 1, L0475: 1, L0598: 1, L0637: 1, L0761: 1, L0766: 1, L0774: 1, L0653: 1, L0659: 1, L0666: 1, L0663: 1, L0664: 1, S0328: 1, H0579: 1, H0521: 1, H0696: 1, H0478: 1, S0432: 1, S0390: 1, L0747: 1, L0756: 1, L0779: 1, L0752: 1, H0445: 1, S0026: 1, S0192: 1,		

		502892	250	48 - 422	574	Gln-18 to Gly-32, Val-84 to Asn-91.	H0543: 1 and H0423: 1.			
31	HE2BW32	609468	41	1 - 228	365		AR089: 28, AR061: 6 H0521: 5, S0222: 2, H0013: 2, H0599: 2, H0622: 2, H0494: 2, S0126: 2, H0624: 1, H0171: 1, S0040: 1, S0420: 1, S0356: 1, S0354: 1, S0360: 1, S0046: 1, H0393: 1, S6022: 1, H0550: 1, H0431: 1, H0586: 1, H0069: 1, H0635: 1, S0280: 1, H0620: 1, H0375: 1, H0594: 1, S0003: 1, S0214: 1, H0591: 1, H0551: 1, H0623: 1, S0144: 1, S0344: 1, S0148: 1, H0547: 1, H0519: 1, H0593: 1, L0602: 1, S0152: 1, S3012: 1, L0740: 1, L0731: 1 and S0194: 1.			
32	HAJAU21	670606	42	2 - 364	366		AR089: 2, AR061: 0 L0769: 2, S0420: 1,	16q23	103850	

33	HE8DL23	693641	43	29 - 406	367	Leu-68 to Gln-77.	AR089: 1, AR061: 0	H0271: 1, H0561: 1 and H0647: 1.	
34	HFTCM92	928851	44	1 - 378	368	Gly-1 to Arg-7, Ala-9 to Ser-15, Ala-25 to Gly-30, Gln-75 to Cys-84, His-111 to Tyr-116.	AR089: 11, AR061: 7 L0766: 6, H0539: 4, L0769: 3, L0748: 3, L0779: 3, L0731: 3, S0360: 2, H0052: 2, H0545: 2, H0494: 2, L0759: 2, L0599: 2, H0295: 1, L0622: 1, L0021: 1, H0530: 1, H0546: 1, H0457: 1, H0086: 1, H0123: 1, H0687: 1, H0551: 1, H0413: 1, L0646: 1, L0768: 1, L0381: 1, L0659: 1, L0783: 1, L0809: 1, L0790: 1, L0666: 1, L0663: 1, H0520: 1, H0670: 1, S3012: 1, L0747: 1, H0445: 1, S0276: 1, H0543: 1, H0423: 1 and H0352: 1.		
		948605	251	826 - 539	575	Gly-10 to Lys-17.			
35	HE6BQ76	775616	45	2 - 298	369	Thr-10 to Ala-21,	AR061: 202, AR089:		

36	HAMFP60	715097	46	2 - 505	370		136	AR089: 9, AR061: 1 L0766: 3, H0633: 2, H0125: 1, H0050: 1, H0560: 1, S0210: 1, L0783: 1, H0435: 1, S0152: 1 and H0521: 1.		
37	HHFHY84	715098	47	3 - 311	371	Pro-30 to Gly-35.		AR089: 11, AR061: 3 L0766: 3, H0633: 2, H0125: 1, H0050: 1, H0560: 1, S0210: 1, L0783: 1, H0435: 1, S0152: 1 and H0521: 1.		
38	HE6FD03	1150900	48	891 - 232	372	Ser-6 to Glu-16, Asp-33 to Lys-38, Glu-71 to Phe-79, Gln-120 to Glu-131, Met-152 to Asp-159, Ala-169 to Pro-174, Leu-182 to Lys-201.		AR089: 1, AR061: 0 H0046: 1, H0674: 1, H0100: 1, L0774: 1, L0659: 1, L0783: 1, L0438: 1, H0659: 1, L0741: 1, L0747: 1, L0786: 1, L0777: 1 and L0758: 1.		
		859840	252	82 - 762	576	Pro-35 to Ser-43, Glu-61 to Phe-69, Gln-110 to Glu-120.				
39	HDTFT90	1165338	49	396 - 1	373	Gln-12 to Gln-17, Arg-64 to Thr-69, Ser-127 to Ser-132.		AR089: 24, AR061: 7 L0665: 8, L0659: 4, L0809: 4, L0731: 4,		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		944518	253		577	Thr-27 to Leu-32, Gly-42 to Gly-56, Ser-80 to Arg-90.			
40	HPJCU63	1082458	50	898 - 461	374	Phe-14 to Pro-20, His-23 to Ile-30, Ala-53 to Thr-58.	AR089: 3, AR061: 2 L0163: 1, L0806: 1, L0788: 1, H0144: 1, S0152: 1 and L0361: 1.			
		904598	254	3 - 848	578	Thr-108 to Gly-115, Val-174 to Gly-181, Ala-205 to Gly-214, Pro-272 to Asn-282.				
41	HFITE38	793203	51	2 - 409	375	Pro-1 to Glu-13, Ser-22 to Lys-28, Gln-39 to Arg-50, Ser-111 to Asp-116.	AR089: 23, AR061: 3 S0196: 4, H0032: 1 and L0769: 1.	Xp11.4-p11.1		300047, 300062, 300600, 309470, 309500, 309610, 310500, 310600, 310600,

42	HDPDH64	796509	52	1 - 303	376	Pro-5 to Lys-22, Arg-43 to Glu-51, Arg-63 to Ala-71, Asp-73 to Lys-79.	AR089: 3, AR061: 1 H0521: 6, H0580: 1, H0012: 1, L0800: 1, H0522: 1 and L0595: 1.			311050, 312060	
43	HFKKS58	1158800	53	2 - 1135	377		AR089: 1, AR061: 1 H0638: 2, L0665: 2, L0747: 2, L0759: 2, H0170: 1, H0686: 1, H0671: 1, H0587: 1, L0622: 1, L0471: 1, H0620: 1, S0250: 1, T0006: 1, H0553: 1, H0673: 1, H0169: 1, H0551: 1, T0067: 1, H0413: 1, H0560: 1, H0538: 1, L0598: 1, L0520: 1, L0764: 1, L0766: 1, L0649: 1, L0375: 1, L0666: 1, L0663: 1, L0664: 1, H0144: 1, H0693: 1, H0659: 1, S0027: 1, L0749: 1, L0756: 1, L0777: 1, L0594: 1, S0276: 1, H0422: 1 and H0352: 1.			

		914398	255	2 - 1135	579	Gln-93 to Gln-100, Thr-206 to Arg-212, Gln-260 to Leu-269, Arg-277 to Asp-284, Arg-350 to Lys-357, Arg-363 to Lys-378.			
44	HE8CM38	1197903	54	2 - 616	378	His-44 to Gly-49, His-148 to Gly-154, Lys-181 to Phe-204.	AR089: 14, AR061: 9 L0803: 6, L0742: 5, S0222: 4, H0599: 4, H0620: 4, L0766: 4, L0748: 4, L0439: 4, L0809: 3, H0555: 3, L0749: 3, S0282: 2, S0354: 2, H0431: 2, H0574: 2, T0039: 2, L0435: 2, L0666: 2, L0665: 2, L0438: 2, L0756: 2, L0753: 2, S0031: 2, L0588: 2, S0356: 1, S0358: 1, S0360: 1, H0393: 1, S6016: 1, H0592: 1, H0643: 1, H0331: 1, H0013: 1, H0156: 1, H0575: 1, H0590: 1, S0010: 1, H0581: 1, S0049: 1, H0327: 1, H0012: 1, H0024: 1,		

		932013	256	2 - 586	580	His-44 to Gly-49, His-148 to Gly-154.	H0014: 1, L0163: 1, S0388: 1, S0051: 1, S6028: 1, H0622: 1, H0032: 1, H0163: 1, H0038: 1, H0413: 1, H0059: 1, L0520: 1, L0770: 1, L0761: 1, L0772: 1, L0643: 1, L0764: 1, L0662: 1, L0767: 1, L0804: 1, L0775: 1, L0805: 1, L0657: 1, L0659: 1, L0790: 1, L0663: 1, L0352: 1, H0547: 1, H0689: 1, H0648: 1, L0751: 1, L0779: 1, L0777: 1, L0758: 1 and L0759: 1.		
45	HAJBU67	856922	55	340 - 729	379	Pro-1 to Arg-8.	AR061: 1, AR089: 1 H0585: 9, H0265: 2, H0141: 2, S0360: 2, H0251: 2, H0031: 2, L0519: 2, L0545: 2, L0664: 2, H0668: 2, S0040: 1, T0049: 1, H0656: 1, H0255: 1,		

46	HHEHD10	1204696	56	481 - 1458	380	Thr-16 to Thr-22, Leu-29 to Met-37, Pro-55 to Gln-64, Ser-69 to Leu-75, Pro-82 to Ser-95, Lys-126 to Val-142, Ser-159 to Leu-172, Arg-174 to Met-181, Thr-189 to Asn-195, Arg-216 to Trp-229, Leu-266 to Gly-272, Ala-283 to Glu-289,	AR089: 25, AR061: 8 H0521: 4, L0770: 3, L0761: 3, L0659: 3, H0341: 2, H0617: 2, L0764: 2, L0766: 2, L0666: 2, L0759: 2, L0589: 2, H0265: 1, H0638: 1, S0360: 1, H0369: 1, H0550: 1, S0222: 1, H0586: 1, H0486: 1, H0250: 1, L0021: 1, H0618: 1,	S0376: 1, S0132: 1, H0546: 1, H0375: 1, S0314: 1, H0428: 1, H0039: 1, H0553: 1, L0055: 1, H0264: 1, H0561: 1, H0509: 1, L0643: 1, L0803: 1, L0651: 1, L0378: 1, L0776: 1, L0659: 1, L0790: 1, L0666: 1, H0519: 1, S0126: 1, H0521: 1, H0576: 1, L0777: 1, L0755: 1, L0731: 1, L0757: 1, L0759: 1, H0665: 1, S0194: 1 and S0458: 1.		

							Gln-310 to Leu-315.	H0253: 1, H0309: 1, H0271: 1, H0039: 1, H0031: 1, H0087: 1, S0142: 1, L0763: 1, L0372: 1, L0644: 1, L0768: 1, L0375: 1, L0805: 1, L0653: 1, L0776: 1, L0655: 1, L0809: 1, L0663: 1, L0665: 1, H0672: 1, H0555: 1, L0612: 1, L0741: 1, L0740: 1, L0747: 1, L0779: 1, L0777: 1, L0731: 1, L0596: 1, S0276: 1 and H0542: 1.		
						581	Pro-3 to Gly-11, Gly-53 to His-63, Leu-70 to Lys-89, Met-99 to Thr-108.			
					894411	257	3 - 428			
47	HHEND45				919630	57	1 - 195	381	Gly-1 to Lys-7.	AR089: 4, AR061: 2 H0543: 2		
48	HE8EQ22				1031960	58	169 - 726	382	Leu-39 to Arg-44.	AR089: 7, AR061: 7 H0013: 2, H0560: 2, H0521: 2, H0624: 1, S6028: 1, S0038: 1, T0042: 1, L0475: 1, H0646: 1, S0426: 1,		

								L0766: 1, H0520: 1, H0519: 1, H0555: 1, H0542: 1 and S0424: 1.		
49	HSACD83	911588	59	1 - 402	383		AR089: 0, AR061: 0 H0497: 1 and T0039: 1.			
50	HHGBO53	1091714	60	681 - 1	384	Glu-20 to Ala-30, Gly-49 to His-62, Ser-75 to Gln-83, Gly-148 to Gly-154, Arg-158 to Ser-167, Pro-169 to Pro-176, Leu-213 to Val-222.	AR089: 9, AR061: 6 H0635: 2, H0333: 1 and H0488: 1.			
		911594	258	169 - 885	582	Leu-39 to Arg-44, Lys-178 to Asp-186.				
		894375	259	1 - 252	583	Gln-5 to Gly-10.				
51	HE8FD82	1154785	61	2 - 826	385	Arg-12 to Gln-23, Asp-82 to Pro-88, Gly-112 to Ala-120, Arg-122 to Arg-127, Gly-172 to Gly-186, Val-212 to Gly-219, Gly-242 to Gly-247, Thr-253 to Ser-265.	AR061: 4, AR089: 3 L0794: 4, S0360: 2, H0553: 2, H0100: 2, L0803: 2, L0741: 2, L0745: 2, H0686: 1, S0212: 1, S0418: 1, S0420: 1, L0534: 1, T0039: 1, H0013: 1, H0575: 1, H0581: 1, H0327: 1, H0428: 1, T0006: 1, H0032: 1, H0207: 1, S0002: 1,			

52	HOHAS44	909634	260	97 - 891	584	Ala-29 to Cys-34.	L0761: 1, L0499: 1, L0383: 1, L0519: 1, L0543: 1, L0789: 1, L0666: 1, H0144: 1, S0126: 1, H0658: 1, H0670: 1, H0436: 1, L0439: 1, L0786: 1, L0759: 1, L0596: 1 and L0592: 1.			
		914810	62	2 - 706	386	Ser-14 to Val-23, Lys-76 to Ser-84, Ser-102 to Leu-109, Gln-119 to Cys-125, Glu-177 to Thr-189, Ala-221 to Phe-231.	AR089: 1, AR061: 0 H0046: 7, H0521: 7, H0052: 6, L0465: 6, H0031: 5, H0624: 4, S0358: 4, H0580: 4, S0010: 4, S0346: 4, H0551: 4, S0212: 3, S0418: 3, S0007: 3, H0437: 3, H0156: 3, H0575: 3, H0457: 3, L0471: 3, T0010: 3, S0250: 3, H0328: 3, H0644: 3, H0040: 3, H0494: 3, S0344: 3, S0002: 3, H0144: 3, L0438: 3, H0520: 3, S0152: 3, H0665: 3, S0001: 2, H0402: 2,		

S0360: 2, S0046: 2,
H0393: 2, H0549: 2,
H0013: 2, H0069: 2,
H0318: 2, H0373: 2,
H0051: 2, S0214: 2,
H0553: 2, S0036: 2,
H0591: 2, H0038: 2,
H0616: 2, L0370: 2,
H0529: 2, H0519: 2,
H0539: 2, L0602: 2,
L0439: 2, L0591: 2,
S0026: 2, H0423: 2,
H0171: 1, L0615: 1,
S0040: 1, H0656: 1,
S0354: 1, H0329: 1,
H0369: 1, H0431: 1,
H0600: 1, H0586: 1,
H0559: 1, H0270: 1,
H0635: 1, H0427: 1,
H0590: 1, T0071: 1,
H0581: 1, N0006: 1,
H0123: 1, H0024: 1,
L0146: 1, H0014: 1,
S0003: 1, H0615: 1,
H0039: 1, H0622: 1,
H0030: 1, H0124: 1,
H0598: 1, H0090: 1,
L0060: 1, H0272: 1,

							S0015: 1, H0561: 1, S0440: 1, H0641: 1, H0646: 1, H0649: 1, S0210: 1, L0520: 1, L0378: 1, L0666: 1, S0374: 1, L0565: 1, H0547: 1, S0146: 1, H0436: 1, H0631: 1, L0779: 1, L0752: 1, S0260: 1, H0707: 1, L0596: 1, L0588: 1, L0485: 1, L0608: 1, L0593: 1, L0594: 1, H0653: 1 and H0422: 1.		
53	HE8OF42	1117857	63	1 - 513	387	Glu-3 to Phe-8, Lys-43 to Glu-48, Gly-62 to Pro-71.	AR089: 30, AR061: 6 H0013: 2 and L0485: 1.		
		810432	261	1 - 513	585	Glu-3 to Phe-8, Lys-43 to Glu-48, Gly-62 to Pro-71.			
54	HSKHS71	1154798	64	1 - 540	388	Ala-94 to Cys-100, Ser-126 to Val-136, Val-161 to Asn-166.	AR089: 6, AR061: 4 S3014: 2		
		911592	262	1 - 381	586	Ala-94 to Cys-100.			
55	HISBT75	1181020	65	606 - 118	389	Pro-5 to Lys-12, Pro-18 to Arg-37, Asn-56 to Gly-63, Ser-75 to Arg-83,	AR089: 6, AR061: 5 L0766: 6, L0748: 3, L0779: 3, S0360: 2, H0545: 2, H0494: 2,		

						Gly-147 to Gly-156.	L0769: 2, L0731: 2, L0759: 2, L0599: 2, H0295: 1, L0622: 1, L0021: 1, H0052: 1, H0546: 1, H0457: 1, H0086: 1, H0123: 1, H0413: 1, L0646: 1, L0768: 1, L0381: 1, L0659: 1, L0783: 1, L0809: 1, L0790: 1, L0666: 1, L0663: 1, H0539: 1, S3012: 1, L0747: 1, S0276: 1, H0543: 1 and H0352: 1.		
				963281	263	3 - 425	587	Ala-8 to Gly-13, Gln-58 to Cys-67, His-94 to Tyr-99, Ser-107 to Ala-112.	
56	HFVKF77	930964	66	3787 - 1541	390	Glu-29 to Leu-37, Ser-47 to Glu-53, Glu-87 to Gln-92, Asn-112 to Ala-119.	AR089: 8, AR061: 7 H0046: 7, H0521: 7, H0052: 6, L0465: 6, H0031: 5, H0624: 4, S0358: 4, H0580: 4, S0010: 4, S0346: 4, H0551: 4, S0212: 3, S0418: 3, S0007: 3, H0437: 3, H0156: 3, H0575: 3, H0457: 3,		

		L0471: 3, T0010: 3, S0250: 3, H0328: 3, H0644: 3, H0040: 3, H0494: 3, S0344: 3, S0002: 3, H0144: 3, L0438: 3, H0520: 3, S0152: 3, H0665: 3, S0001: 2, H0402: 2, S0360: 2, S0046: 2, H0393: 2, H0549: 2, H0013: 2, H0069: 2, H0318: 2, H0373: 2, H0051: 2, S0214: 2, H0553: 2, S0036: 2, H0591: 2, H0038: 2, H0616: 2, L0370: 2, H0529: 2, H0519: 2, H0539: 2, L0602: 2, L0439: 2, L0591: 2, S0026: 2, H0423: 2, H0171: 1, L0615: 1, S0040: 1, H0656: 1, S0354: 1, H0329: 1, H0369: 1, H0431: 1, H0600: 1, H0586: 1, H0559: 1, H0270: 1, H0635: 1, H0427: 1, H0590: 1, T0071: 1,					

							H0581: 1, N0006: 1, H0123: 1, H0024: 1, L0146: 1, H0014: 1, S0003: 1, H0615: 1, H0039: 1, H0622: 1, H0030: 1, H0124: 1, H0598: 1, H0090: 1, L0060: 1, H0272: 1, S0015: 1, H0561: 1, S0440: 1, H0641: 1, H0646: 1, H0649: 1, S0210: 1, L0520: 1, L0378: 1, L0666: 1, S0374: 1, L0565: 1, H0547: 1, S0146: 1, H0436: 1, H0631: 1, L0779: 1, L0752: 1, S0260: 1, H0707: 1, L0596: 1, L0588: 1, L0485: 1, L0608: 1, L0593: 1, L0594: 1, H0653: 1 and H0422: 1.		
57	HJABW64	931402	67	1 - 465	391	Ala-26 to Thr-33, Ser-52 to Glu-58, Thr-83 to Leu-92.	AR061: 3, AR089: 2 H0266: 4, L0588: 4, L0592: 4, L0595: 4, H0144: 3, S0046: 2, H0013: 2, S0003: 2, L0766: 2, H0519: 2,		

						H0539: 2, L0750: 2, L0777: 2, L0758: 2, L0759: 2, S0242: 2, S0424: 2, H0624: 1, S0040: 1, S0420: 1, L0005: 1, S0356: 1, H0357: 1, H0052: 1, H0009: 1, H0570: 1, S0051: 1, H0038: 1, H0413: 1, T0069: 1, T0041: 1, H0494: 1, L0369: 1, L0794: 1, L0649: 1, L0803: 1, L0650: 1, L0651: 1, L0666: 1, H0520: 1, H0435: 1, H0658: 1, H0666: 1, H0214: 1, S0028: 1, L0439: 1, L0755: 1 and L0593: 1.		
58	HCEMY90	932927	68	49 - 606	392		AR089: 0, AR061: 0 H0090: 2, H0052: 1 and L0439: 1.		
59	HHFLF63	933854	69	1 - 669	393	Gly-1 to Trp-7, Gln-47 to Ser-54, Glu-105 to Asn-110, Thr-115 to Asp-123, Glu-147 to Asp-152, Glu-161 to Asn-167,	AR061: 9, AR089: 7 L0766: 3, H0457: 2, H0551: 2, H0529: 2, L0527: 2, H0144: 2, S0152: 2, H0521: 2, L0759: 2, H0343: 2,		

					Pro-188 to Lys-195.	H0542: 2, H0624: 1, H0306: 1, H0619: 1, L0586: 1, H0013: 1, H0635: 1, H0327: 1, H0615: 1, H0591: 1, S0002: 1, L0796: 1, L0805: 1, L0791: 1, L0745: 1, L0750: 1, L0780: 1, L0731: 1, L0599: 1 and H0422: 1.	
60	HSKAN19	935229	70	34 - 1212	394	Arg-1 to Glu-8, Ser-249 to Glu-254.	AR061: 9, AR089: 4 L0731: 8, L0803: 4, L0665: 3, L0756: 3, S0358: 2, L0637: 2, L0662: 2, L0666: 2, L0777: 2, L0595: 2, H0170: 1, H0662: 1, L0005: 1, S0222: 1, H0409: 1, H0486: 1, S0388: 1, H0428: 1, H0561: 1, S0450: 1, H0538: 1, H0529: 1, L0800: 1, L0764: 1, L0794: 1, L0766: 1, L0774: 1, L0659: 1, L0783: 1, L0663: 1, L0664: 1, H0521: 1, H0436: 1, S3014: 1,

61	HE9SE88	1152240	71	554 - 3	395	Leu-88 to Pro-94, His-164 to Pro-174.		S0027: 1, L0748: 1, L0755: 1, L0759: 1, H0445: 1, L0591: 1, H0543: 1 and H0506: 1.			
								AR061: 6, AR089: 3 H0013: 1, H0144: 1 and H0521: 1.			
		894905	264	1 - 408	588						
62	HDTDG41	942490	72	197 - 580	396			AR089: 26, AR061: 5 L0731: 10, L0105: 7, S0360: 6, H0171: 5, H0251: 5, H0624: 4, L0794: 4, L0659: 4, H0144: 4, H0170: 3, H0486: 3, L0803: 3, H0013: 2, L0750: 2, L0777: 2, L0755: 2, L0581: 2, H0661: 1, S0376: 1, H0329: 1, L0717: 1, H0369: 1, H0587: 1, H0427: 1, H0309: 1, H0123: 1, L0471: 1, L0163: 1, H0039: 1, H0622: 1, H0163: 1, H0379: 1, L0598: 1, L0763: 1, L0662: 1, L0664: 1, H0658: 1, S0380: 1,			

63	HTEPX32	870698	73	91 - 699	397	Ser-10 to Gly-15, Pro-20 to Ser-27, Glu-34 to Gly-41, Ala-45 to Trp-50, Pro-79 to Gly-88.	S0332: 1, S0028: 1, S0192: 1, S0196: 1 and S0458: 1.	AR089: 11, AR061: 2 H0038: 6, H0616: 6, L0794: 4, L0768: 1 and L0758: 1.		
64	HEGAB84	1128320	74	475 - 17	398		AR089: 13, AR061: 8 H0618: 2 and H0550: 1.			
		823900	265	1 - 351	589	Ile-30 to Gly-36, Thr-67 to Thr-72.				
65	HTEKQ12	1213746	75	1 - 1869	399	Gly-15 to Arg-21, Pro-30 to Ser-35, Ser-44 to Asp-51, Pro-109 to Phe-115, Glu-131 to Ser-139, Arg-166 to Ser-179, Gly-205 to Gly-215, Ser-234 to Arg-252, Arg-279 to Glu-288, Leu-355 to Cys-362, Glu-371 to His-376, Thr-393 to Asp-401, Arg-506 to Asn-512, Asp-571 to Lys-578, Pro-580 to Pro-592,	AR089: 1, AR061: 0 H0253: 27, H0618: 21, H0038: 14, L0439: 13, L0758: 5, H0616: 4, L0794: 4, L0803: 4, H0556: 2, L0438: 2, L0608: 2, H0265: 1, H0676: 1, H0559: 1, H0355: 1, H0510: 1, H0375: 1, H0617: 1, H0413: 1, H0647: 1, H0646: 1, L0644: 1, L0773: 1, L0774: 1, L0790: 1, H0520: 1, H0547: 1, H0690: 1,			

66	HNTSX71	1221117	76	230 - 1417	400	Ser-26 to Val-32, Ala-60 to Trp-66.	AR089: 15, AR061: 2 S0126: 4, H0135: 3, H0494: 3, H0547: 3, S0045: 2, H0550: 2, H0545: 2, H0242: 2, H0266: 2, H0551: 2, H0653: 2, S0040: 1, S0282: 1, S0358: 1, S0376: 1, S0046: 1, H0393: 1, S6022: 1, H0549: 1, H0156: 1, H0618: 1, H0253: 1, H0123: 1, H0050: 1, H0024: 1, H0014: 1, H0252: 1, H0124: 1, H0040: 1, H0623: 1, S0370: 1, S0210: 1, L0648: 1, L0518: 1, S0374: 1, H0435: 1, S0328: 1, S0152: 1 and S0404: 1.	L0779: 1, H0543: 1 and H0506: 1.		
		947964	266	2 - 472	590	Ser-9 to Asp-16, Pro-74 to Phe-80, Lys-85 to Gly-91.	Lys-601 to Leu-608.				
		963289	267	2 - 436	591	Pro-6 to Arg-14, Gly-97 to Asp-109,					

							Pro-118 to Cys-123, Cys-135 to Ser-140.				
		974741	268		649 - 206	592	Pro-9 to Arg-17, Gly-100 to Asp-112, Pro-121 to Cys-126, Cys-138 to Ser-143.				
67	HFCFH75	951202	77		2 - 646	401	Ser-75 to Lys-80, Arg-167 to Lys-172.				AR089: 9, AR061: 7 H0266: 4, L0588: 4, L0592: 4, L0595: 4, H0144: 3, S0046: 2, H0013: 2, S0003: 2, L0766: 2, H0519: 2, H0539: 2, L0750: 2, L0777: 2, L0758: 2, L0759: 2, S0242: 2, S0424: 2, H0624: 1, S0040: 1, S0420: 1, L0005: 1, S0356: 1, H0357: 1, H0052: 1, H0009: 1, H0570: 1, S0051: 1, H0038: 1, H0413: 1, T0069: 1, T0041: 1, H0494: 1, L0369: 1, L0794: 1, L0649: 1, L0803: 1, L0650: 1, L0651: 1, L0666: 1, H0520: 1, H0435: 1, H0658: 1,

68	HEOQY55	1204693	78	1323 - 1	402	Ser-15 to Cys-21, Leu-52 to Ser-58, Gly-161 to Glu-167, Arg-282 to Arg-289, Ser-340 to Gln-345, Arg-375 to Gln-381, Gly-392 to Ala-399, Pro-401 to Trp-406.	H0666: 1, H0214: 1, S0028: 1, L0439: 1, L0755: 1 and L0593: 1.	AR089: 1, AR061: 1 L0748: 15, L0439: 6, H0457: 4, H0009: 3, H0620: 3, L0438: 3, S0212: 2, H0559: 2, H0673: 2, H0690: 2, H0265: 1, H0341: 1, H0305: 1, S0418: 1, S0360: 1, S0045: 1, S0140: 1, S0278: 1, H0549: 1, T0109: 1, H0069: 1, H0590: 1, H0618: 1, T0048: 1, H0581: 1, H0052: 1, H0050: 1, L0185: 1, H0271: 1, H0213: 1, H0617: 1, H0040: 1, H0551: 1, H0264: 1, L0769: 1, L0638: 1, L0761: 1, L0644: 1, L0771: 1, L0649: 1, L0657: 1, L0809: 1, L0666: 1, L0665: 1, H0519: 1, H0689: 1, H0435: 1, S0044: 1,		

								S0390: 1, S0037: 1, S3014: 1, L0742: 1, L0754: 1, L0747: 1, H0543: 1 and H0422: 1.		
		883406	269	73 - 840	593	Gly-5 to Arg-12, Ile-52 to Thr-61, Val-85 to Gly-92, Tyr-114 to Thr-121, Lys-133 to Pro-138, Thr-186 to Arg-192.				
69	HPJDQ48	952185	79	194 - 559	403	Arg-1 to Ser-14, Glu-46 to Glu-51.		AR089: 12, AR061: 3 L0766: 3, H0633: 2, H0125: 1, H0050: 1, H0560: 1, L0783: 1, S0152: 1 and H0521: 1.		
70	HTTCB17	1174865	80	8 - 2041	404	Ala-1 to Gly-12.		AR061: 7, AR089: 4 L0766: 8, L0748: 7, H0038: 4, H0543: 4, L0779: 3, H0624: 2, S0007: 2, H0083: 2, L0805: 2, L0666: 2, H0547: 2, L0439: 2, L0777: 2, L0758: 2, L0596: 2, L0599: 2, S0026: 2, H0657: 1, S0212: 1, H0255: 1, S0420: 1, S0358: 1, S0444: 1, S0360: 1,		

							H0431: 1, S0414: 1, H0004: 1, S0010: 1, H0597: 1, H0546: 1, H0354: 1, H0266: 1, H0383: 1, H0361: 1, H0040: 1, H0616: 1, L0151: 1, H0264: 1, H0560: 1, L0520: 1, L0640: 1, L0638: 1, L0794: 1, L0803: 1, L0375: 1, L0806: 1, L0655: 1, L0663: 1, H0520: 1, H0519: 1, H0670: 1, H0672: 1, S0146: 1, H0555: 1, L0752: 1, L0731: 1, L0759: 1, S0031: 1, H0445: 1, L0595: 1 and L0366: 1.		
		948595	270	2942 - 909	594	Ala-1 to Gly-12.			
71	HE2SY09	953828	81	2 - 646	405	Asp-1 to Glu-11, Arg-23 to Asp-29.	AR061: 1, AR089: 1 H0521: 3, H0624: 1, H0650: 1, S0001: 1, H0437: 1, H0052: 1, H0056: 1, H0519: 1, S0028: 1 and S0031: 1.		
72	HFEBN52	810429	82	1 - 450	406	Asn-50 to Gly-56, Cys-95 to Gly-103.	AR089: 16, AR061: 11 H0150: 1 and H0081:		

73	HCHMO62	955551	83	3 - 362	407	Gln-102 to Pro-108.	1. AR089: 10, AR061: 4 H0341: 1 and H0484: 1.			
74	HHSDM19	956045	84	1789 - 1730	408		AR061: 3, AR089: 2 H0266: 4, L0588: 4, L0592: 4, L0595: 4, H0144: 3, S0046: 2, H0013: 2, S0003: 2, L0766: 2, H0519: 2, H0539: 2, L0750: 2, L0777: 2, L0758: 2, L0759: 2, S0242: 2, S0424: 2, H0624: 1, S0040: 1, S0420: 1, L0005: 1, S0356: 1, H0357: 1, H0052: 1, H0009: 1, H0570: 1, S0051: 1, H0038: 1, H0413: 1, T0069: 1, T0041: 1, H0494: 1, L0369: 1, L0794: 1, L0649: 1, L0803: 1, L0650: 1, L0651: 1, L0666: 1, H0520: 1, H0435: 1, H0658: 1, H0666: 1, H0214: 1, S0028: 1, L0439: 1,		

75	HDTIT49	956917	85	854 - 3	409	Lys-93 to Gln-98, Asp-141 to Leu-148, Asn-166 to Pro-172, Glu-174 to Gln-179, Ser-187 to Lys-192, Gln-221 to Gln-229, Pro-239 to Asp-246.	L0755: 1 and L0593: 1.		
							AR089: 1, AR061: 0 L0803: 8, S0414: 6, L0740: 6, L0757: 5, L0439: 4, L0747: 4, L0759: 4, S0412: 4, H0486: 3, L0598: 3, L0770: 3, L0662: 3, L0794: 3, L0775: 3, L0655: 3, L0666: 3, L0731: 3, L0599: 3, S0114: 2, S0212: 2, H0024: 2, S0003: 2, H0328: 2, H0615: 2, H0070: 2, H0591: 2, H0059: 2, L0768: 2, L0665: 2, L0438: 2, H0659: 2, H0658: 2, S0330: 2, L0746: 2, L0756: 2, L0758: 2, L0362: 2, H0170: 1, H0656: 1, L0808: 1, S0356: 1, S0354: 1, S0358: 1, S0360: 1, T0008: 1, H0013: 1, H0069: 1, H0156: 1, H0599: 1, H0098: 1, H0575: 1, S0346: 1,		

							T0115: 1, H0046: 1, H0563: 1, H0373: 1, L0163: 1, H0316: 1, H0551: 1, T0041: 1, H0652: 1, S0422: 1, L0369: 1, L0638: 1, L0637: 1, L0761: 1, L0521: 1, L0363: 1, L0766: 1, L0649: 1, L0804: 1, L0784: 1, L0806: 1, L0805: 1, L0659: 1, L0787: 1, L0788: 1, L0792: 1, L0663: 1, S0052: 1, H0144: 1, H0519: 1, S0126: 1, H0684: 1, H0435: 1, H0670: 1, H0518: 1, H0521: 1, H0696: 1, H0555: 1, L0748: 1, L0779: 1, L0752: 1, S0242: 1, H0543: 1, H0423: 1, S0424: 1 and H0506: 1.		
76	HTLGW19	1163072	86	3 - 1034	410	Val-52 to Arg-57, Ala-128 to Asp-134, Val-148 to Glu-154, Gln-290 to Leu-298.	AR061: 5, AR089: 3 L0770: 2, L0766: 2, L0803: 2, L0439: 2, L0751: 2, L0757: 2, H0422: 2, L0785: 1,		

									S0360: 1, H0619: 1, S0278: 1, H0250: 1, H0618: 1, H0253: 1, T0110: 1, H0050: 1, S0051: 1, S0250: 1, H0252: 1, H0615: 1, H0212: 1, H0264: 1, L0351: 1, H0560: 1, S0144: 1, L0762: 1, L0378: 1, L0806: 1, L0653: 1, L0659: 1, L0790: 1, S0126: 1, H0690: 1, H0521: 1, H0576: 1, S0028: 1, L0779: 1, L0780: 1 and L0758: 1.		
		788606	271	261 - 1553	595	Val-51 to Arg-56, Ala-127 to Asp-133, Val-147 to Glu-153.					
77	HJPCA88	958942	87	2 - 562	411	Gly-8 to Cys-13, Gln-38 to Met-48, Arg-76 to Gln-82, Cys-87 to Asp-94.	AR061: 0, AR089: 0 S0116: 1, H0438: 1, H0083: 1, S0364: 1, H0560: 1 and H0539: 1.				
78	HE9TA54	960253	88	2 - 1399	412	Cys-22 to Cys-31, Leu-35 to Pro-54, Gln-59 to Glu-73, Arg-131 to Met-140, Asn-149 to Arg-156,	AR089: 9, AR061: 9 H0251: 12, H0013: 6, L0759: 5, H0351: 4, H0373: 4, H0529: 4, L0766: 4, L0754: 4,				

						Ser-191 to Thr-196, Leu-299 to Leu-313, Glu-328 to Pro-336, Val-393 to Asp-399, Asn-454 to Asn-466.	L0750: 4, L0777: 4, L0666: 3, H0684: 3, L0439: 3, S0442: 2, H0318: 2, H0553: 2, H0551: 2, H0412: 2, T0042: 2, S0422: 2, L0649: 2, H0144: 2, H0539: 2, L0731: 2, L0757: 2, H0445: 2, L0592: 2, L0608: 2, H0624: 1, H0685: 1, H0656: 1, H0306: 1, L0005: 1, S0356: 1, H0261: 1, H0550: 1, H0592: 1, H0587: 1, H0635: 1, H0581: 1, H0421: 1, H0052: 1, H0263: 1, H0546: 1, L0471: 1, L0163: 1, H0083: 1, H0594: 1, H0622: 1, H0068: 1, H0634: 1, H0379: 1, H0264: 1, T0041: 1, H0494: 1, H0560: 1, H0633: 1, L0769: 1, L0772: 1, L0764: 1, L0771: 1, L0773: 1, L0662: 1, L0794: 1,		

							L0388: 1, L0522: 1, L0803: 1, L0629: 1, L0657: 1, L0519: 1, L0789: 1, L0663: 1, L0665: 1, S0374: 1, H0547: 1, H0365: 1, H0670: 1, S0330: 1, S0378: 1, S0152: 1, S3014: 1, S0027: 1, L0747: 1, L0749: 1, L0601: 1, H0653: 1, H0543: 1 and H0422: 1.	
79	HCFCD40	963756	89	1355 - 3004	413	Gln-11 to Glu-19, Ser-61 to Ser-71, Ser-76 to Ser-84, Pro-111 to Ser-124, Ala-153 to Ser-161, Ser-177 to Gly-182, Asp-197 to Asn-205, Ser-219 to Ser-225.	AR089: 4, AR061: 2 L0439: 7, L0748: 6, L0747: 6, L0749: 6, H0013: 4, H0265: 3, H0556: 3, S0360: 3, H0581: 3, L0471: 3, H0622: 3, L0662: 3, H0543: 3, S0218: 2, S0358: 2, L0717: 2, S0222: 2, H0486: 2, H0263: 2, H0545: 2, H0040: 2, H0056: 2, L0770: 2, L0517: 2, L0666: 2, H0519: 2, L0602: 2, S0027: 2, L0740: 2, L0754: 2,	

L0759: 2, L0596: 2,
H0542: 2, S0134: 1,
L0415: 1, H0341: 1,
S0212: 1, H0663: 1,
S0418: 1, S0354: 1,
H0637: 1, S0007: 1,
H0208: 1, S0132: 1,
H0619: 1, H0393: 1,
H0586: 1, H0587: 1,
H0574: 1, T0039: 1,
S0280: 1, H0036: 1,
S0049: 1, H0196: 1,
H0046: 1, H0123: 1,
H0023: 1, L0163: 1,
T0010: 1, H0615: 1,
T0006: 1, H0031: 1,
H0553: 1, H0032: 1,
H0551: 1, H0623: 1,
T0041: 1, H0494: 1,
H0560: 1, H0633: 1,
H0538: 1, L0769: 1,
L0667: 1, L0646: 1,
L0800: 1, L0767: 1,
L0768: 1, L0766: 1,
L0774: 1, L0775: 1,
L0375: 1, L0776: 1,
L0606: 1, L0657: 1,
L0659: 1, L0543: 1,

							L0647: 1, L0791: 1, L0663: 1, S0053: 1, L0565: 1, L0352: 1, H0520: 1, H0547: 1, H0435: 1, H0539: 1, H0521: 1, S0028: 1, S0206: 1, L0741: 1, L0756: 1, L0779: 1, L0731: 1, L0757: 1, L0758: 1, S0260: 1, L0605: 1, H0653: 1, H0667: 1, H0422: 1 and H0506: 1.		
80	HHBEN77	1189720	90	2 - 1009	414	Pro-1 to Asp-10, Arg-24 to Leu-42, Val-65 to Ser-75, Arg-95 to Asp-104, Glu-111 to Ile-119, Asp-151 to Arg-157, His-212 to Leu-222, Ala-251 to Gly-256, His-309 to Ala-314, Gly-321 to Gln-331.	AR089: 3, AR061: 3 H0599: 45, S0364: 8, H0002: 3, S0366: 3, L0803: 3, L0622: 2, L0623: 2, H0016: 2, L0604: 2, H0097: 1, H0122: 1, H0196: 1, H0373: 1, H0553: 1, H0040: 1, H0634: 1, L0769: 1 and L0783: 1.	
		951627	272	2 - 790	596	Pro-1 to Asp-10, Arg-24 to Leu-42, Val-65 to Ser-75, Arg-95 to Asp-104, Glu-111 to Ile-119,			

						Asp-151 to Arg-157.			
81	HHESP66	1154641	91	111 - 830	415	Lys-1 to Ser-18, Asn-49 to Glu-62, Gln-67 to Ser-76, Glu-84 to Thr-90, Thr-104 to Pro-112, Ser-148 to Arg-156, Gly-184 to Thr-191, Pro-203 to Glu-210, Thr-234 to Ser-240.	AR061: 2, AR089: 2 L0766: 6, L0665: 4, H0650: 2, H0402: 2, S0360: 2, L0794: 2, L0803: 2, L0592: 2, S0134: 1, S0278: 1, H0251: 1, H0263: 1, H0321: 1, H0591: 1, H0551: 1, S0422: 1, L0645: 1, L0764: 1, L0809: 1, L0788: 1, L0666: 1, L0663: 1, S0052: 1, H0547: 1, H0134: 1, S0404: 1, H0478: 1, L0740: 1, L0754: 1, L0779: 1, L0777: 1, L0755: 1, L0758: 1, H0543: 1 and S0384: 1.		
		919192	273	107 - 667	597	Lys-1 to Ser-18, Asn-49 to Glu-62, Gln-67 to Ser-76, Glu-84 to Thr-90, Thr-104 to Pro-112.			
82	HAHHQ37	967442	92	59 - 1993	416	Leu-35 to Lys-41, Leu-61 to Glu-68, Ser-153 to Gln-158,	AR061: 2, AR089: 1 H0618: 4, H0584: 3, H0592: 3, H0253: 3,		

						Asn-223 to Pro-228, Ala-259 to Phe-266, Pro-276 to Gly-283, Asp-292 to Phe-307, Ala-318 to Asp-336, Pro-348 to Leu-365, Ala-369 to Thr-393, Gln-398 to Ala-408.	H0587: 2, H0599: 2, H0457: 2, H0521: 2, H0583: 1, H0484: 1, H0402: 1, S0354: 1, S0358: 1, H0590: 1, H0634: 1, H0529: 1, H0697: 1, L0750: 1, H0136: 1, H0423: 1 and H0677: 1.		
83	HAMAA10	968749	93	73 - 972	417	Gly-4 to Ala-19.	AR089: 1, AR061: 0 L0604: 6, L0485: 2, L0623: 1, H0122: 1, H0373: 1, L0809: 1 and L0584: 1.		
84	HHFMH12	969324	94	2 - 2170	418	Asp-21 to Tyr-27, Pro-66 to Leu-72, Glu-99 to Ala-105, Gly-111 to Val-120, Gln-132 to Ile-138, Asp-152 to Ala-159, Lys-165 to Arg-170, Thr-222 to Cys-229, Arg-265 to Tyr-270, Ser-274 to Asp-283, Asp-299 to Ser-306, Val-316 to Arg-322, Asp-333 to Lys-346, Ser-447 to Arg-452,	AR061: 3, AR089: 1 L0601: 7, H0622: 4, S0380: 4, S0356: 3, T0010: 3, S0038: 3, L0769: 3, S0360: 2, L0157: 2, H0623: 2, S0306: 2, L0770: 2, L0662: 2, L0659: 2, S3014: 2, L0759: 2, H0556: 1, H0295: 1, S0114: 1, S0134: 1, S0046: 1, S0132: 1, H0619: 1, H0393: 1, L0717: 1, S0222: 1,		

	Asn-589 to Glu-594.	S6014: 1, H0370: 1, H0586: 1, T0040: 1, H0635: 1, H0036: 1, T0048: 1, H0052: 1, H0194: 1, H0263: 1, H0231: 1, H0050: 1, H0023: 1, H0014: 1, H0083: 1, H0266: 1, S0250: 1, L0483: 1, H0048: 1, H0321: 1, S0036: 1, H0040: 1, H0634: 1, H0551: 1, H0272: 1, H0433: 1, H0412: 1, H0413: 1, H0100: 1, T0041: 1, H0494: 1, S0144: 1, S0210: 1, L0803: 1, L0655: 1, L0809: 1, L0663: 1, H0691: 1, H0520: 1, H0519: 1, H0435: 1, S0044: 1, S0027: 1, L0742: 1, L0748: 1, L0749: 1, L0756: 1, L0777: 1, L0753: 1, L0731: 1, L0758: 1, L0366: 1, H0665: 1, S0242: 1, S0194: 1, H0543: 1 and				

							H0008: 1.		
85	HDTIE58	971339	95	393 - 2315	419	Ser-9 to Cys-21, Asn-137 to Leu-142, Gly-231 to Thr-236, Arg-284 to Phe-291, Asn-305 to Asp-313, Ala-375 to Asn-383, Cys-404 to Arg-411, Val-456 to Glu-469, Glu-516 to Leu-521, Lys-572 to Tyr-588.	AR089: 4, AR061: 3 S0045: 1, H0600: 1, H0486: 1 and L0809: 1.		
86	HIBCN93	973679	96	207 - 938	420	Met-26 to Asn-37, Glu-42 to Gln-51, Thr-68 to Ser-95, Ala-97 to Lys-113, Asp-156 to Val-161, Val-208 to Asp-215, Pro-217 to Ala-228.	AR089: 2, AR061: 1 L0740: 12, L0439: 10, L0766: 7, L0769: 4, L0794: 4, L0756: 4, H0549: 3, L0768: 3, L0803: 3, L0665: 3, S0206: 3, L0750: 3, H0423: 3, S0007: 2, S0010: 2, S0346: 2, H0052: 2, H0327: 2, H0024: 2, H0051: 2, L0763: 2, L0770: 2, H0144: 2, L0758: 2, H0556: 1, L0760: 1, S6026: 1, S0300: 1, H0550: 1, S0222: 1, H0392: 1, H0331: 1,	6q21-q23.2	107470, 107470, 107470, 120110, 121014, 164200, 164200, 601316, 601666, 601757, 602772

87	HSWAP86	1165386	97	253 - 786	421	Pro-5 to Lys-12, Pro-18 to Arg-37, Asn-56 to Gly-63, Ser-75 to Arg-83.	H0013: 1, H0318: 1, S0049: 1, H0194: 1, H0103: 1, H0050: 1, L0471: 1, H0620: 1, H0373: 1, S0388: 1, T0010: 1, H0399: 1, H0553: 1, H0644: 1, H0032: 1, H0124: 1, H0068: 1, S0036: 1, H0135: 1, H0038: 1, H0616: 1, H0551: 1, T0067: 1, H0100: 1, H0560: 1, H0561: 1, L0662: 1, L0649: 1, L0774: 1, L0517: 1, L0809: 1, L0647: 1, L0789: 1, L0792: 1, L0352: 1, S0126: 1, H0539: 1, S0380: 1, H0518: 1, S0004: 1, S0044: 1, S3014: 1, L0748: 1, L0747: 1, L0686: 1, L0592: 1, S0196: 1 and H0352: 1.	AR089: 3, AR061: 2 L0766: 6, L0748: 3, L0779: 3, S0360: 2, H0545: 2, H0494: 2,		

							L0769: 2, L0731: 2, L0759: 2, L0599: 2, H0295: 1, L0622: 1, L0021: 1, H0052: 1, H0546: 1, H0457: 1, H0086: 1, H0123: 1, H0413: 1, L0646: 1, L0768: 1, L0381: 1, L0659: 1, L0783: 1, L0809: 1, L0790: 1, L0666: 1, L0663: 1, H0539: 1, S3012: 1, L0747: 1, S0276: 1, H0543: 1 and H0352: 1.		
		947000	274	3 - 281	598	Thr-1 to Pro-8, Gln-42 to Cys-51, His-78 to Tyr-83.			
		948606	275	737 - 477	599				
88	HHSGI32	1216549	98	3 - 1745	422	Ser-36 to Gln-43, Ala-109 to Ser-123, Leu-147 to Glu-157, Pro-173 to Thr-178, Thr-197 to Thr-202, Lys-208 to Asn-222, Gly-230 to Asp-252, Glu-262 to Gly-274, Glu-304 to Arg-311, His-420 to Gly-425,	AR061: 2, AR089: 1 L0803: 6, L0742: 5, H0599: 4, H0620: 4, L0766: 4, L0748: 4, L0439: 4, S0222: 3, L0809: 3, L0749: 3, S0282: 2, T0039: 2, L0435: 2, L0666: 2, L0665: 2, L0438: 2, L0756: 2, L0753: 2,		

His-524 to Gly-530, Lys-557 to Phe-580.	S0031: 2, L0588: 2, S0356: 1, S0354: 1, S0358: 1, S0360: 1, H0393: 1, S6016: 1, H0431: 1, H0592: 1, H0643: 1, H0331: 1, H0574: 1, H0013: 1, H0575: 1, H0590: 1, S0010: 1, H0581: 1, S0049: 1, H0327: 1, H0012: 1, H0024: 1, H0014: 1, L0163: 1, S0388: 1, S0051: 1, S6028: 1, H0622: 1; H0032: 1, H0163: 1, H0038: 1, H0413: 1, H0059: 1, L0520: 1, L0770: 1, L0761: 1, L0772: 1, L0643: 1, L0764: 1, L0662: 1, L0767: 1, L0804: 1, L0775: 1, L0805: 1, L0657: 1, L0659: 1, L0790: 1, L0663: 1, L0352: 1, H0547: 1, H0689: 1, H0648: 1, H0555: 1, L0751: 1, L0779: 1, L0777: 1,			

								L0758: 1 and L0759: 1.			
		958555	276	142 - 1194	600		Leu-33 to Gln-39.				
89	HAJBH69	812164	99	3 - 323	423		Asn-15 to Glu-24.	AR089: 2, AR061: 2 H0253: 7, L0794: 7, L0761: 5, L0758: 5, H0402: 4, S0358: 3, H0586: 3, H0618: 3, H0457: 3, S0002: 3, L0766: 3, L0774: 3, L0659: 3, L0666: 3, H0484: 2, H0551: 2, L0770: 2, L0764: 2, L0649: 2, H0684: 2, H0670: 2, H0539: 2, H0696: 2, L0748: 2, L0779: 2, H0543: 2, H0306: 1, S0420: 1, L0617: 1, H0580: 1, S0046: 1, H0261: 1, H0592: 1, H0485: 1, H0590: 1, T0048: 1, H0318: 1, H0421: 1, H0052: 1, H0530: 1, H0179: 1, H0188: 1, H0622: 1, H0617: 1, H0124: 1, H0135: 1, H0038: 1, H0264: 1, H0413: 1, H0623: 1,	22q13.31	250100, 250800, 250800

							L0351: 1, H0494: 1, H0561: 1, H0641: 1, S0422: 1, L0763: 1, L0769: 1, L0667: 1, L0646: 1, L0800: 1, L0643: 1, L0644: 1, L0771: 1, L0662: 1, L0768: 1, L0386: 1, L0533: 1, L0806: 1, L0653: 1, L0657: 1, L0664: 1, H0691: 1, H0518: 1, H0521: 1, S0404: 1, H0436: 1, L0743: 1, L0777: 1 and L0600: 1.		
90	HAGFN07	953606	100	797 - 357	424		AR089: 38, AR061: 7 L0731: 2 and S0010: 1.		
91	HFRBZ64	575037	101	217 - 660	425	Glu-51 to Phe-60, Gln-63 to Gly-73, Thr-85 to Lys-91.	AR089: 3, AR061: 0 S0001: 1, S0050: 1 and H0181: 1.		
92	HMAER78	702735	102	3 - 272	426	Asp-77 to Lys-82.	AR061: 243, AR089: 175 S0050: 1, S0144: 1, S0052: 1 and S0028: 1.		
93	HKAAV49	1179713	103	1 - 1923	427	Pro-1 to Lys-13, Pro-20 to Lys-39, Ala-46 to Thr-71, Pro-112 to Gln-122,	AR089: 11, AR061: 2 L0766: 14, L0761: 3, L0792: 3, L0779: 3, L0717: 2, H0135: 2,		

94	HAPQS74	855538	104	774 - 415	428	Thr-15 to Glu-20, Val-29 to Arg-39,	Glu-5 to Lys-10, Pro-17 to Lys-36, Ala-43 to Thr-68, Pro-109 to Gln-119, Gly-126 to Arg-148, Gly-156 to Ile-161, Ala-185 to Asp-192.	961297	277	188 - 796	601	Gly-129 to Arg-151, Gly-159 to Ile-164, Ala-188 to Tyr-194, Asn-208 to Pro-217, Gly-237 to Thr-249, Gly-267 to Ala-285, Ser-292 to Phe-303, Lys-305 to Ala-319, Asp-330 to Arg-337, Leu-347 to Asn-358, Val-368 to Ala-378, Thr-390 to Asp-395, Ser-417 to Arg-445, Phe-449 to Leu-476, Ala-510 to Lys-532, Ser-546 to Glu-562, Lys-570 to Ser-589, Val-609 to Glu-623.	AR089: 4, AR061: 4 L0766: 10, L0752: 8,	H0264: 2, L0809: 2, L0790: 2, L0791: 2, L0666: 2, L0591: 2, S0134: 1, H0650: 1, H0657: 1, H0483: 1, H0580: 1, H0486: 1, H0013: 1, H0575: 1, H0590: 1, H0581: 1, H0050: 1, H0024: 1, S0364: 1, H0163: 1, L0351: 1, T0042: 1, H0494: 1, H0633: 1, S0422: 1, S0002: 1, L0770: 1, L0769: 1, L0796: 1, L0764: 1, L0662: 1, L0794: 1, L0804: 1, L0606: 1, L0783: 1, L0777: 1, S0194: 1 and H0543: 1.		

							L0439: 6, L0747: 6, L0740: 5, L0756: 5, L0779: 4, L0777: 4, L0731: 4, S0051: 3, L0803: 3, L0774: 3, L0754: 3, S0360: 2, H0574: 2, L0763: 2, L0805: 2, L0809: 2, L0663: 2, L0751: 2, L0755: 2, L0759: 2, L0601: 2, H0624: 1, S0040: 1, S0298: 1, S0420: 1, H0580: 1, H0351: 1, H0600: 1, H0331: 1, H0013: 1, L0021: 1, H0575: 1, H0590: 1, T0110: 1, H0012: 1, H0615: 1, H0031: 1, H0553: 1, H0591: 1, H0646: 1, S0002: 1, L0772: 1, L0645: 1, L0773: 1, L0662: 1, L0794: 1, L0381: 1, L0775: 1, L0776: 1, L0657: 1, L0659: 1, L0528: 1, L0790: 1, L0666: 1, H0547: 1, H0648: 1,
						Pro-58 to Arg-66, Lys-95 to Phe-105, Val-109 to Ala-114.	

							H0539: 1, S0152: 1, H0696: 1, S0044: 1, S0028: 1, L0758: 1, L0366: 1, S0011: 1, S0276: 1, H0422: 1 and S0424: 1.		
95	HTEPM33	870561	105	1 - 735	429	Pro-8 to Gly-26, Cys-54 to Cys-66, Gly-73 to His-85.	AR061: 25, AR089: 5 L0758: 3, H0616: 2, H0038: 1 and L0779: 1.		
96	HLTES49	872262	106	2 - 280	430	Ser-31 to Gly-43, Ser-45 to Gly-57.	AR089: 20, AR061: 7 H0090: 2, H0419: 1, H0483: 1, H0459: 1, S0045: 1, H0455: 1, H0642: 1, H0485: 1, H0486: 1, H0052: 1, H0239: 1, H0617: 1, T0042: 1, H0494: 1, H0641: 1, H0547: 1, S0044: 1, S0037: 1, L0742: 1, L0439: 1, L0755: 1 and H0543: 1.		
97	HDTEJ81	919873	107	1 - 474	431	Ser-37 to Gly-49, Ser-51 to Gly-63, Val-93 to Cys-98.	AR089: 1, AR061: 0 L0747: 13, L0755: 8, L0731: 8, L0750: 7, H0657: 6, L0758: 6, L0769: 4, H0617: 3, L0764: 3, L0439: 3, L0752: 3, H0090: 2,		

H0641: 2, L0651: 2,
L0776: 2, L0809: 2,
H0144: 2, L0740: 2,
L0749: 2, L0759: 2,
S0276: 2, H0656: 1,
H0419: 1, H0483: 1,
H0459: 1, H0125: 1,
S0360: 1, S0045: 1,
H0455: 1, H0587: 1,
H0642: 1, H0485: 1,
H0486: 1, L0021: 1,
H0318: 1, H0052: 1,
H0544: 1, H0046: 1,
H0239: 1, H0687: 1,
H0606: 1, H0674: 1,
H0059: 1, L0351: 1,
T0042: 1, H0494: 1,
S0144: 1, S0426: 1,
L0770: 1, L0643: 1,
L0771: 1, L0521: 1,
L0767: 1, L0766: 1,
L0551: 1, L0803: 1,
L0774: 1, L0775: 1,
L0655: 1, L0518: 1,
L0782: 1, L0783: 1,
L0383: 1, L0519: 1,
L0528: 1, L0789: 1,
S0052: 1, S0374: 1,

									L0352: 1, H0547: 1, H0666: 1, S0044: 1, S0037: 1, L0742: 1, L0748: 1, L0751: 1, L0780: 1, L0683: 1, L0599: 1 and H0543: 1.		
98	HTLCY21	910212	108	68 - 556	432	Leu-12 to Ser-19, Glu-108 to Ser-119, Ala-121 to Thr-128, Lys-139 to Ala-149, Arg-153 to Ala-161.			AR061: 1, AR089: 0 L0741: 2, H0618: 1, H0253: 1 and H0668: 1.		
99	HKAKF45	1090988	109	1 - 840	433	Gln-43 to Ser-49, Ala-60 to Gly-67.			AR061: 3, AR089: 2 H0494: 2 and H0690: 1.		
		911611	278	1 - 582	602	Gln-43 to Ser-49, Ala-60 to Gly-67, Arg-141 to Pro-146.					
100	HMWDF88	906769	110	147 - 362	434	Trp-14 to Asp-27.			AR061: 207, AR089: 155 H0341: 1 and H0083: 1.		
101	HHECU86	945062	111	1 - 585	435	Asp-15 to Leu-21, Ser-59 to His-66, Ile-159 to Tyr-164.			AR089: 5, AR061: 2 S0126: 3, H0551: 2, L0770: 2, L0748: 2, L0740: 2, H0542: 2, H0556: 1, S0116: 1, S0420: 1, S0360: 1, H0575: 1, H0581: 1,	6	

102	HTPHO01	1152424	112	868 - 2	436	Thr-7 to Pro-18, Thr-235 to Gly-240.	AR061: 4, AR089: 3 H0599: 25, L0731: 19, L0750: 14, L0754: 13, L0766: 8, L0776: 8, L0752: 8, L0757: 8, L0747: 6, L0744: 5, L0769: 4, L0779: 4, L0777: 4, S0420: 3, L0770: 3, L0755: 3, L0758: 3, L0471: 2, L0771: 2, L0775: 2, L0806: 2, L0659: 2, S0126: 2, H0670: 2, L0743: 2, L0759: 2, L0604: 2, H0624: 1, H0685: 1, H0650: 1, H0484: 1, H0483: 1, H0661: 1, S0358: 1, S0360: 1, S0046: 1, H0411: 1, H0632: 1, H0427: 1, S0280: 1, H0097: 1, H0004: 1, S0049: 1, H0028: 1,	H0050: 1, H0641: 1, L0766: 1, L0649: 1, S0390: 1, L0745: 1, L0731: 1, L0593: 1 and H0543: 1.		

							H0622: 1, L0142: 1, H0591: 1, L0763: 1, L0772: 1, L0800: 1, L0764: 1, L0662: 1, L0768: 1, L0794: 1, L0774: 1, L0807: 1, L0809: 1, L0666: 1, L0665: 1, S0148: 1, S0328: 1, S0406: 1, S3014: 1, S0027: 1, S0028: 1, L0599: 1, S0026: 1 and H0667: 1.		
		912348	279	1 - 639	603	Ile-11 to Arg-20, Pro-56 to Ala-69, Ser-81 to Glu-86, Asp-108 to Trp-116, Pro-142 to Gly-158, Cys-207 to Ser-213.	AR061: 3, AR089: 2 L0777: 8, H0549: 7, L0665: 6, L0751: 6, L0809: 5, L0439: 5, S0116: 3, S0354: 3, H0620: 3, H0083: 3, L0803: 3, L0774: 3, L0805: 3, L0659: 3, L0666: 3, H0696: 3, L0779: 3, L0601: 3,		
103	HFXKR90	948399	113	589 - 2	437				

H0423: 3, H0656: 2, S0282: 2, H0483: 2, H0619: 2, H0486: 2, S0049: 2, H0309: 2, H0316: 2, L0763: 2, L0767: 2, L0776: 2, L0655: 2, L0657: 2, L0438: 2, H0520: 2, H0658: 2, L0602: 2, H0555: 2, H0624: 1, H0686: 1, H0295: 1, S0114: 1, H0657: 1, H0255: 1, S0358: 1, S0360: 1, H0340: 1, H0580: 1, S0046: 1, H0455: 1, H0333: 1, H0574: 1, H0559: 1, T0109: 1, H0156: 1, L0021: 1, T0074: 1, H0618: 1, H0318: 1, S0474: 1, H0581: 1, H0052: 1, H0327: 1, H0530: 1, H0562: 1, H0012: 1, H0687: 1, S0250: 1, H0615: 1, H0428: 1, L0483: 1, H0553: 1, H0673: 1, H0135: 1, H0059: 1,						

							S0038: 1, H0494: 1, L0065: 1, H0207: 1, L0520: 1, L0640: 1, L0769: 1, L0638: 1, L0637: 1, L0761: 1, L0771: 1, L0521: 1, L0662: 1, L0629: 1, L0526: 1, L0368: 1, L0789: 1, L0663: 1, L0664: 1, H0519: 1, H0593: 1, H0682: 1, H0659: 1, H0670: 1, H0518: 1, H0521: 1, H0522: 1, S0176: 1, H0478: 1, L0748: 1, L0740: 1, L0750: 1, L0755: 1, L0731: 1, S0436: 1, L0608: 1, L0362: 1, S0026: 1, H0667: 1, S0242: 1 and H0543: 1.		
104	HDPBQ32	949191	114	3 - 1004	438		AR061: 0, AR089: 0 L0439: 19, L0766: 10, H0521: 10, L0550: 7, L0731: 7, L0666: 6, L0748: 5, L0599: 5, S0116: 4, H0575: 4, H0617: 4, L0770: 4,	

L0774: 4, L0438: 4,
L0740: 4, L0745: 4,
L0747: 4, L0759: 4,
L0604: 4, L0471: 3,
L0769: 3, L0662: 3,
L0775: 3, L0783: 3,
H0435: 3, L0750: 3,
L0756: 3, L0777: 3,
L0752: 3, H0657: 2,
H0661: 2, H0663: 2,
H0486: 2, H0427: 2,
H0581: 2, H0052: 2,
H0032: 2, L0455: 2,
S0002: 2, L0761: 2,
L0776: 2, L0657: 2,
L0659: 2, L0518: 2,
H0520: 2, H0519: 2,
H0689: 2, H0670: 2,
H0522: 2, L0746: 2,
L0605: 2, L0485: 2,
H0667: 2, H0543: 2,
H0423: 2, H0624: 1,
H0170: 1, H0265: 1,
H0556: 1, H0685: 1,
S0218: 1, L0443: 1,
S0212: 1, S0001: 1,
S0348: 1, S0358: 1,
S0360: 1, H0580: 1,

	S0046: 1, H0619: 1, S0222: 1, H0592: 1, H0497: 1, H0574: 1, H0632: 1, L0586: 1, L0021: 1, H0318: 1, H0046: 1, H0572: 1, H0024: 1, S0051: 1, T0010: 1, H0083: 1, S6028: 1, H0266: 1, H0271: 1, T0023: 1, L0483: 1, H0031: 1, H0673: 1, S0366: 1, H0135: 1, H0090: 1, H0038: 1, H0488: 1, H0268: 1, H0412: 1, H0059: 1, S0386: 1, H0560: 1, S0150: 1, S0144: 1, S0344: 1, H0538: 1, S0426: 1, H0529: 1, L0369: 1, L0640: 1; L0763: 1, L0637: 1, L0667: 1, L0646: 1, L0641: 1, L0626: 1, L0768: 1, L0387: 1, L0376: 1, L0632: 1, L0806: 1, L0655: 1, L0809: 1, L0787: 1, L0792: 1,					

							L0663: 1, H0691: 1, H0660: 1, H0648: 1, H0672: 1, S0328: 1, S0378: 1, S0044: 1, S0188: 1, H0134: 1, S3012: 1, S0390: 1, S0028: 1, L0749: 1, L0786: 1, L0779: 1, L0755: 1, L0757: 1, L0758: 1, L0608: 1, H0665: 1, H0542: 1 and S0384: 1.	
105	HNTAR73	949289	115	2 - 376	439	Pro-11 to Ala-17, Pro-19 to Gly-27, Cys-60 to Gln-71, Arg-73 to His-83, Pro-85 to Asn-92.	AR061: 1, AR089: 1 H0549: 7, L0665: 6, L0751: 6, L0439: 5, H0620: 3, L0803: 3, L0777: 3, L0601: 3, H0483: 2, H0486: 2, H0309: 2, L0774: 2, L0657: 2, L0659: 2, L0809: 2, L0666: 2, L0438: 2, H0520: 2, H0658: 2, L0602: 2, H0555: 2, H0624: 1, H0686: 1, H0295: 1, H0656: 1, S0282: 1, H0255: 1, S0354: 1, H0580: 1, H0619: 1,	

						H0618: 1, H0581: 1, S0049: 1, H0052: 1, H0562: 1, H0012: 1, H0083: 1, H0687: 1, S0250: 1, H0428: 1, L0483: 1, H0135: 1, S0038: 1, H0494: 1, L0640: 1, L0638: 1, L0637: 1, L0771: 1, L0662: 1, L0805: 1, L0655: 1, L0629: 1, L0368: 1, L0789: 1, L0663: 1, H0519: 1, H0593: 1, H0682: 1, H0670: 1, H0521: 1, H0522: 1, H0696: 1, L0740: 1, L0779: 1, H0667: 1 and H0543: 1.		
106	HHEGC16	950778	116	1178 - 861	440		AR089: 19, AR061: 2 L0770: 2, S0126: 2, L0748: 2, L0740: 2, H0542: 2, S0420: 1, S0360: 1, H0575: 1, H0551: 1, L0766: 1, L0745: 1, L0731: 1 and H0543: 1.		
107	HSIGE72	952275	117	2 - 1663	441	Glu-1 to Ser-7.	AR061: 6, AR089: 4 L0803: 6, L0748: 6,		

108	HCGMG56	953660	118	706 - 170	442	Gln-24 to Pro-43, Gly-68 to Lys-74.	L0439: 6, L0777: 5, L0438: 3, S0330: 3, L0749: 3, S0282: 2, H0615: 2, L0770: 2, L0646: 2, L0754: 2, L0750: 2, L0756: 2, L0779: 2, S0031: 2, L0592: 2, L0485: 2, S0035: 1, H0574: 1, T0109: 1, H0013: 1, H0244: 1, H0590: 1, S0346: 1, H0421: 1, H0052: 1, T0110: 1, S0050: 1, S0003: 1, H0644: 1, H0383: 1, H0169: 1, L0455: 1, H0598: 1, L0370: 1, L0598: 1, L0521: 1, L0662: 1, L0804: 1, L0774: 1, L0775: 1, L0653: 1, L0518: 1, L0788: 1, H0144: 1, H0660: 1, H0704: 1, L0742: 1, L0740: 1, L0759: 1, H0217: 1 and H0543: 1.	AR089: 9, AR061: 5 H0090: 2, H0419: 1,	

							H0483: 1, H0459: 1, S0045: 1, H0455: 1, H0642: 1, H0485: 1, H0486: 1, H0052: 1, H0239: 1, H0617: 1, T0042: 1, H0494: 1, H0641: 1, H0547: 1, S0044: 1, S0037: 1, L0742: 1, L0439: 1, L0755: 1 and H0543: 1.		
109	HNGBQ66	966001	119	252 - 1532	443	Lys-34 to Ala-42, Lys-71 to Leu-76, Arg-188 to Trp-193, Val-215 to Asn-220, Ser-269 to Gln-274, Leu-333 to Lys-341, Thr-354 to Lys-361, Thr-401 to Ile-407, Lys-419 to Arg-427.	AR089: 52, AR061: 12 H0556: 1, H0346: 1, S0358: 1, H0090: 1, T0042: 1, H0560: 1, S0052: 1, H0519: 1 and S0152: 1.		
110	HTXPY09	966013	120	312 - 617	444	Ser-9 to Asn-15, Ser-64 to Gln-69.	AR061: 1, AR089: 1 H0581: 2, H0556: 1 and H0538: 1.		
111	HCHAS12	966626	121	1 - 1209	445	Cys-1 to Arg-13, Pro-15 to Gly-21, Gly-54 to Ser-59.	AR061: 15, AR089: 4 H0617: 41, L0754: 38, L0779: 38, L0758: 32, H0618: 17, H0483: 11, S0358: 10, L0775: 10, L0777: 7, H0484: 6,		

L0774: 6, L0776: 6, L0748: 6, L0740: 6, L0752: 6, H0253: 5, H0181: 5, T0114: 4, L0750: 4, L0780: 4, L0755: 4, H0606: 3, H0087: 3, L0769: 3, L0764: 3, L0771: 3, L0806: 3, H0295: 2, S0354: 2, H0549: 2, H0298: 2, H0590: 2, H0510: 2, H0553: 2, H0038: 2, H0494: 2, H0509: 2, L0783: 2, L0809: 2, L0789: 2, L0665: 2, S0330: 2, H0696: 2, L0747: 2, L0596: 2, H0653: 2, H0661: 1, S0376: 1, H0282: 1, H0331: 1, H0574: 1, H0575: 1, H0251: 1, H0263: 1, H0204: 1, H0596: 1, T0110: 1, H0597: 1, H0327: 1, L0719: 1, H0544: 1, H0545: 1, H0178: 1, H0620: 1, H0375: 1, H0188: 1,							

								H0615: 1, H0622: 1, H0033: 1, H0424: 1, H0644: 1, L0640: 1, L0763: 1, L0761: 1, L0772: 1, L0800: 1, L0642: 1, L0773: 1, L0662: 1, L0767: 1, L0794: 1, L0766: 1, L0649: 1, L0525: 1, L0659: 1, L0782: 1, L0666: 1, L0663: 1, L0565: 1, H0682: 1, H0670: 1, H0521: 1, L0741: 1, L0743: 1, L0439: 1, L0786: 1, L0731: 1, L0601: 1 and H0423: 1.		
112	H6EDI12	1154053	122	3 - 557	446	Pro-30 to Ala-37, Ala-40 to Arg-49, Ala-152 to Leu-163.	AR089: 1, AR061: 0 S0294: 2, H0559: 1 and L0747: 1.			
		911587	280	1 - 549	604	Pro-28 to Ala-35, Ala-38 to Arg-47.				
113	HE8MI76	911474	123	230 - 961	447	Pro-12 to Ala-17, Asp-23 to Phe-28.	AR089: 3, AR061: 0 S0040: 2, H0547: 2, L0393: 1, H0013: 1, H0427: 1, T0110: 1, T0078: 1, S0364: 1, H0124: 1, H0551: 1,			

114	HSDGJ23	714160	124	148 - 405	448		H0100: 1, H0494: 1, H0509: 1, H0555: 1 and L0439: 1.			
							AR061: 0, AR089: 0 H0255: 1, H0305: 1, S0044: 1, S0037: 1, S0028: 1 and S0031: 1.			
115	HHSAD81	602854	125	607 - 386	449	Ser-9 to Glu-14, Arg-22 to Arg-27.	AR061: 1, AR089: 1 H0494: 2, H0544: 1, S0051: 1, L0754: 1 and H0542: 1.			
		847391	281	1781 - 1107	605	Arg-164 to Arg-169.				
		970432	282	1 - 678	606					
116	HCEEZ56	1171692	126	3 - 1346	450	Lys-10 to Arg-25, Glu-40 to Ala-46, Arg-174 to Ala-181, Ala-202 to Gln-208.	AR061: 3, AR089: 2 H0618: 3, L0439: 3, H0124: 2, L0771: 2, L0766: 2, S0126: 2, H0445: 2, H0265: 1, H0253: 1, H0318: 1, H0421: 1, H0052: 1, H0197: 1, H0015: 1, S6028: 1, H0266: 1, H0380: 1, H0529: 1, L0803: 1, H0144: 1, L0352: 1, S0328: 1, H0539: 1, S0378: 1, H0134: 1, L0749: 1, L0777: 1, L0758: 1 and			

							L0595: 1.			
		971572	283	3 - 1346	607	Lys-10 to Arg-25, Glu-40 to Ala-46, Arg-174 to Ala-181, Ala-202 to Gln-208.				
117	HE8TT33	1189455	127	3 - 2189	451	Leu-26 to Tyr-32, Pro-108 to Gln-123.	AR061: 6, AR089: 4 S0045: 2, S0046: 1, H0645: 1, H0013: 1, H0575: 1, H0286: 1, H0521: 1 and H0136: 1.			
		952123	284	3 - 2189	608	Leu-26 to Tyr-32, Pro-108 to Gln-123.				
118	HAGBX32	951351	128	3 - 509	452	Gly-14 to Glu-32, Pro-60 to Ala-70, Thr-145 to Gly-153, Ser-164 to Leu-169.	AR061: 4, AR089: 4 L0439: 4, L0418: 1, S0010: 1, L0455: 1, S0028: 1 and L0741: 1.			108730, 147781, 172471, 186580, 264800, 266600, 278760, 600760, 600760, 600761, 600761, 602066
		956281	285	473 - 138	609	Phe-4 to Gly-12.				
119	HLWEE80	1202534	129	601 - 1134	453	Ser-38 to Asp-46, Leu-55 to Leu-60,	AR061: 8, AR089: 7 H0081: 2, H0549: 1,			

							Lys-73 to Glu-79.	H0069: 1, H0046: 1, H0428: 1, H0553: 1, H0087: 1, H0529: 1, L0532: 1, H0521: 1 and H0423: 1.		
		840952	286	275 - 688	610	Ser-1 to Trp-6, Ser-10 to Glu-22, Pro-112 to Ser-117.				
120	HMEFI81	1226739	130	141 - 3506	454	Gln-15 to Asn-20, Met-59 to Gln-66.	AR061: 1, AR089: 1 L0748: 11, L0749: 6, L0779: 4, L0438: 2, H0547: 2, L0747: 2, L0777: 2, L0596: 2, H0650: 1, H0013: 1, H0581: 1, H0046: 1, H0009: 1, H0266: 1, H0622: 1, T0042: 1, S0002: 1, H0695: 1, H0529: 1, L0762: 1, L0769: 1, L0771: 1, L0766: 1, L0376: 1, L0809: 1, L0666: 1, L0665: 1, H0658: 1, H0648: 1, S0044: 1, H0555: 1, H0187: 1, L0750: 1, L0752: 1, L0758: 1, H0343: 1, S0026: 1, S0192: 1,		

								S0194: 1, H0542: 1, H0543: 1 and H0423: 1.		
		574258	287	29 - 496	611	Gln-15 to Asn-20, Met-59 to Asp-64.				
121	HOUHW83	1199942	131	79 - 813	455	Thr-1 to Asp-7, Gly-37 to Asn-44, Arg-175 to Tyr-180, Lys-190 to Pro-198, Gln-204 to Leu-209.	AR089: 10, AR061: 3 H0560: 2, S0342: 1, H0586: 1, L0471: 1, H0644: 1, H0617: 1, H0040: 1, H0641: 1, H0529: 1, H0519: 1, S0037: 1 and L0757: 1.			
		882335	288	60 - 680	612	Thr-1 to Asp-7, Gly-37 to Asn-44.				
122	HSLCB60	1193050	132	835 - 284	456	Arg-58 to Glu-63, Val-80 to Gly-87, Arg-114 to Lys-119, Ala-132 to Gly-137, Val-140 to Asp-145, Ala-173 to Pro-178.	AR089: 0 S3010: 2, S0028: 1 and S0260: 1.			
		730740	289	82 - 468	613	Ala-25 to Thr-31, Glu-58 to Arg-63, Gln-82 to Arg-87.				
123	HSLFG64	1228145	133	808 - 2142	457	Arg-1 to Gly-8, His-33 to Glu-44, Ala-57 to Gly-62, Tyr-71 to Arg-77, Pro-85 to Asn-93,	AR089: 1, AR061: 1 S0028: 3, H0617: 2, S0045: 1, H0181: 1, H0383: 1 and S0144: 1.			

						Asp-116 to Ser-122.			
		853387	290	1196 - 3	614	Arg-1 to Gly-8, His-33 to Glu-44, Ala-57 to Gly-62, Tyr-71 to Arg-77, Pro-85 to Asn-93, Asp-116 to His-121.			
124	HTPFX16	974296	134	3 - 422	458	Asp-40 to Asn-49, Cys-65 to Gly-71.	AR061: 3, AR089: 2 L0750: 2, H0024: 1, H0039: 1, H0622: 1, H0040: 1 and S0434: 1.		
125	HWAER24	934693	135	677 - 2566	459	Ser-6 to Thr-11.	AR061: 1, AR089: 0 L0748: 11, L0749: 6, L0779: 4, L0438: 2, H0547: 2, L0747: 2, L0777: 2, L0596: 2, H0650: 1, H0013: 1, H0581: 1, H0046: 1, H0009: 1, H0266: 1, H0622: 1, T0042: 1, S0002: 1, H0695: 1, H0529: 1, L0762: 1, L0769: 1, L0771: 1, L0766: 1, L0376: 1, L0809: 1, L0666: 1, L0665: 1, H0658: 1, H0648: 1, S0044: 1, H0555: 1, H0187: 1,		

							L0750: 1, L0752: 1, L0758: 1, H0343: 1, S0026: 1, S0192: 1, S0194: 1, H0542: 1, H0543: 1 and H0423: 1.		
126	HKMAC08	1121865	136	193 - 723	460	Phe-5 to Val-11, Ser-28 to Lys-35, His-119 to Gln-127.	AR089: 40, AR061: 37 S0015: 1 and H0665: 1.		
		960388	291	193 - 723	615	Phe-5 to Val-11, Ser-28 to Lys-35, His-119 to Gln-127.			
127	HSLHS93	1105323	137	1 - 156	461		AR089: 56, AR061: 55 S0001: 1, S0051: 1 and S0028: 1.		
		791608	292	3 - 143	616				
128	HBGOT10	963457	138	3 - 437	462	Ser-19 to Asp-32, Tyr-58 to Gly-67.	AR061: 2, AR089: 1 S0278: 1, H0031: 1, H0617: 1 and S0390: 1.		
129	HSDJW73	882817	139	358 - 2	463	Val-33 to Tyr-44.	AR089: 1, AR061: 0 H0013: 1, S0028: 1 and S0260: 1.		
		883338	293	221 - 739	617	Arg-52 to Lys-57, Glu-67 to Ile-74.			
130	HWMEQ37	949568	140	97 - 867	464	Leu-29 to Pro-47, Pro-55 to Arg-60, Pro-99 to Gly-106, Met-170 to Thr-177,	AR089: 5, AR061: 2 S0356: 1, S0354: 1, S0358: 1, S0376: 1, H0620: 1, H0023: 1,		

						Glu-196 to Ser-207.	H0039: 1 and H0593: 1.		
131	HFRBX44	1107898	141	249 - 1685	465	Arg-6 to Gly-14, Cys-20 to Gly-27, Leu-80 to Pro-86.	AR089: 1, AR061: 1 S0050: 1, H0316: 1, S0428: 1, H0694: 1 and S0031: 1.		
		860207	294	2 - 292	618	Pro-6 to Thr-15, Asp-27 to Thr-35.			
132	HRDDR74	1103362	142	2 - 646	466	Arg-8 to Arg-14.	AR061: 3, AR089: 2 H0542: 2, H0597: 1, H0288: 1, H0124: 1, H0264: 1, S0344: 1, L0752: 1 and L0581: 1.		
		531702	295	67 - 372	619	Pro-21 to Ser-27, Arg-42 to Asp-49, Arg-82 to Ser-90.			
133	HPIAQ70	1151503	143	564 - 151	467	Arg-12 to Tyr-23, Ser-31 to Pro-37, Thr-42 to Ala-56, Ile-122 to Lys-128.	AR089: 18, AR061: 9 S0150: 1		
		973604	296	185 - 436	620	Gly-36 to Thr-41.			
134	HROAZ07	973603	144	5 - 514	468		AR089: 1, AR061: 0 H0316: 1		
135	HTTER50	1220586	145	1 - 1236	469	Pro-1 to Gly-6, Ile-40 to Lys-46.	AR061: 3, AR089: 2 L0748: 12, L0749: 7, L0766: 5, L0803: 4, L0756: 4, L0769: 3, L0666: 3, H0547: 3,		

136	HUFBV44	1220585	146	3 - 338	470	Gln-13 to Leu-20, Ala-23 to Leu-29, Lys-58 to Tyr-69.	L0777: 3, H0543: 3, S0036: 2, H0040: 2, H0059: 2, L0659: 2, L0790: 2, L0439: 2, H0295: 1, H0657: 1, H0341: 1, S0282: 1, H0228: 1, H0589: 1, S0360: 1, H0431: 1, H0370: 1, H0013: 1, H0156: 1, H0590: 1, H0052: 1, H0051: 1, H0083: 1, S6028: 1, H0188: 1, T0041: 1, H0560: 1, L0643: 1, L0662: 1, L0805: 1, L0776: 1, L0663: 1, H0144: 1, S0328: 1, L0741: 1, L0740: 1, L0751: 1, L0747: 1, L0755: 1, L0758: 1, S0031: 1, H0422: 1 and H0506: 1.	AR089: 2, AR061: 1 L0748: 12, L0749: 7, L0766: 5, L0803: 4,	
		724581	297	263 - 613	621				

137	HE2EI69	534587	147	307 - 14	471	Thr-16 to Lys-25.	L0662: 1, L0805: 1, L0776: 1, L0663: 1, H0144: 1, S0328: 1, L0741: 1, L0740: 1, L0751: 1, L0747: 1, L0755: 1, L0758: 1, S0031: 1, H0422: 1 and H0506: 1.		AR061: 2, AR089: 2 H0170: 2 and S0050: 1.		
138	HWMJR63	1152429	148	3 - 1004	472	Thr-1 to Ile-12,	L0756: 4, L0769: 3, L0666: 3, H0547: 3, L0777: 3, H0543: 3, S0036: 2, H0040: 2, H0059: 2, L0659: 2, L0790: 2, L0439: 2, H0295: 1, H0657: 1, H0341: 1, S0282: 1, H0228: 1, H0589: 1, S0360: 1, H0431: 1, H0370: 1, H0013: 1, H0156: 1, H0590: 1, H0052: 1, H0051: 1, H0083: 1, S6028: 1, H0188: 1, T0041: 1, H0560: 1, L0643: 1,		AR089: 1, AR061: 1		

						Pro-78 to Lys-86, Cys-88 to Leu-97, Asp-100 to Ile-107, Pro-176 to Pro-181, Arg-191 to Met-196, Pro-200 to Arg-210, Pro-246 to Ala-259, Ser-271 to Glu-276, Asp-298 to Trp-306.	H0599: 25, L0731: 19, L0750: 14, L0754: 13, L0766: 8, L0776: 8, L0752: 8, L0757: 8, L0747: 6, L0744: 5, L0769: 4, L0779: 4, L0777: 4, S0420: 3, L0770: 3, L0755: 3, L0758: 3, L0471: 2, L0771: 2, L0775: 2, L0806: 2, L0659: 2, S0126: 2, H0670: 2, L0743: 2, L0759: 2, L0604: 2, H0624: 1, H0685: 1, H0650: 1, H0484: 1, H0483: 1, H0661: 1, S0358: 1, S0360: 1, S0046: 1, H0411: 1, H0632: 1, H0427: 1, S0280: 1, H0097: 1, H0004: 1, S0049: 1, H0028: 1, H0622: 1, L0142: 1, H0591: 1, L0763: 1, L0772: 1, L0800: 1, L0764: 1, L0662: 1, L0768: 1, L0794: 1, L0774: 1, L0807: 1,		

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		922134	299	2 - 1036	623	Pro-1 to Pro-6, Pro-77 to Lys-85, Cys-87 to Leu-96, Asp-99 to Ile-106, Pro-175 to Pro-180, Arg-190 to Met-195, Pro-199 to Arg-209, Pro-245 to Ala-258, Ser-270 to Glu-275, Asp-297 to Trp-305, Gly-334 to Ser-339.			
139	HSLFD83	667155	149	18 - 365	473	Val-11 to Ile-16, Gly-98 to Pro-103.	AR089: 33, AR061: 10 S0028: 2 and H0178: 1.		
140	HBKDA90	912285	150	818 - 531	474	Ser-24 to Ser-29.	AR089: 3, AR061: 1 L0604: 12, S0366: 7, L0485: 5, H0599: 4, L0777: 4, H0196: 3, H0373: 3, L0520: 3, L0623: 2, S0330: 2, H0486: 1, H0013: 1, H0002: 1, H0253: 1, H0318: 1, L0163: 1,		

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		952737	300	292 - 1932	624	Asp-27 to His-32, Gln-65 to Gly-76, Lys-80 to Ser-94, Pro-99 to Asn-104, Gly-126 to Lys-143, Pro-150 to Lys-156, Glu-163 to Glu-175, Val-193 to Asp-204, Met-230 to Ser-263, Ala-278 to Gly-291, Pro-306 to Asn-320, Asn-328 to Lys-333, Glu-348 to Glu-355, Ile-358 to Asn-363, Glu-375 to Ser-381, Lys-390 to Arg-395, Lys-433 to Asn-441, Ser-456 to Phe-463, Glu-484 to Lys-490, Glu-498 to Gly-507, Glu-535 to Glu-547.			
		956567	301	506 - 141	625				
141	HTLAA37	754641	151	2 - 316	475		AR089: 27, AR061: 12 L0761: 4, H0677: 4, H0556: 3, H0661: 3, H0617: 3, H0580: 2,		

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142	HTRAA36	756908	152	220 - 714	476					
		827518	302	3 - 530	626	Arg-21 to Asp-28, Thr-36 to Val-43,				

143	HRGDD16	877117	153	3 - 293	477	Asn-95 to Ser-100.	His-1 to Asp-6, Pro-63 to Leu-74.	AR089: 11, AR061: 4 H0550: 1, S0366: 1 and H0134: 1.		
144	HNSAB28	881286	154	2 - 838	478	Asp-1 to Lys-7, Gly-27 to Gln-32, Arg-67 to Gly-77.		AR089: 6, AR061: 1 H0478: 3, S0278: 2, L0731: 2, S0001: 1, S0360: 1, S0132: 1, H0619: 1, H0263: 1, S0036: 1, H0040: 1, H0494: 1, S0142: 1, S0344: 1, L0764: 1, L0766: 1, S3014: 1, L0748: 1, H0445: 1 and S0434: 1.	12q13	107777, 123940, 139350, 139350, 148040, 148041, 148043, 148070, 231550, 600194, 600231, 600536, 600808, 600956, 601284, 601769, 601769, 601928, 602116, 602153
145	HTTEP70	917729	155	46 - 858	479	Asn-60 to Gln-74, Pro-97 to Arg-103, Pro-128 to Gln-134, Ser-141 to Glu-154,		AR061: 6, AR089: 3 H0623: 3, H0620: 2, H0521: 2, H0542: 2, H0556: 1, H0341: 1,		

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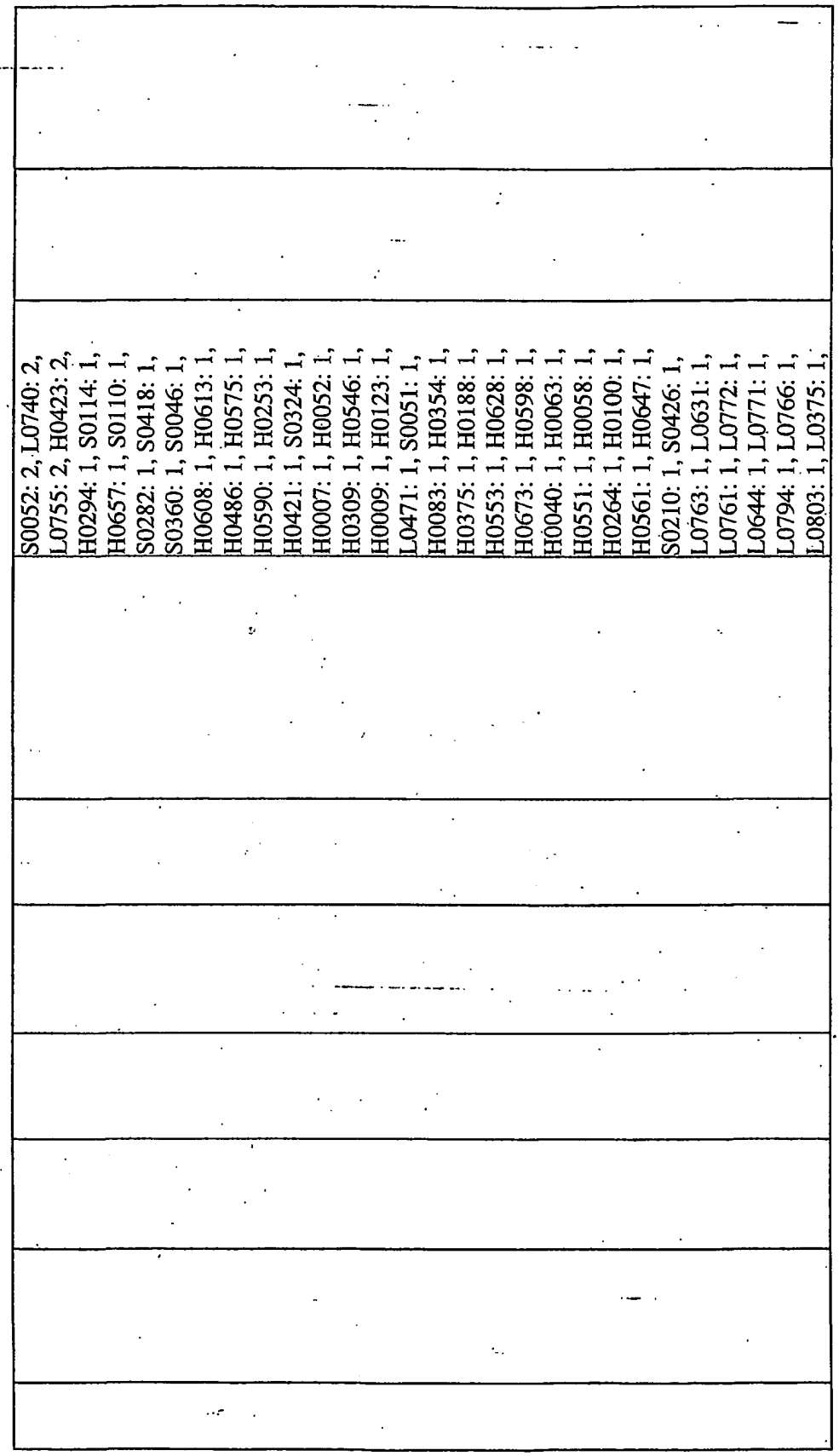
146	HMSII43	946985	156	56 - 517	480	Asn-18 to Gly-25, Lys-33 to Ser-43, His-54 to Cys-63, Ser-71 to Gly-76, Ser-85 to Gln-93.	AR089: 2, AR061: 1 L0731: 17, L0777: 16, L0748: 12, L0751: 10, H0620: 9, L0770: 8, S0002: 7, L0769: 7, L0665: 7, L0747: 6, L0759: 6, H0457: 5, H0012: 4, L0779: 4, S0358: 3, H0050: 3, H0641: 3, L0438: 3, H0225: 2, S0212: 2, H0255: 2, H0638: 2, S0007: 2, H0645: 2, S0278: 2, H0581: 2, H0023: 2, H0051: 2, H0266: 2, S0144: 2, L0667: 2, L0783: 2,		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147	HMADV11	920770	157	21 - 428	481		L0805: 1, L0657: 1, L0659: 1, L0782: 1, L0809: 1, L0790: 1, L0663: 1, L0664: 1, S0428: 1, S0053: 1, S0374: 1, H0547: 1, H0684: 1, H0660: 1, S0330: 1, H0521: 1, S0037: 1, S0206: 1, L0439: 1, H0445: 1, L0599: 1, H0543: 1 and L0462: 1.			
148	HNTCK35	1226201	158	1 - 1842	482	Asp-1 to Gly-9, Arg-62 to Asp-68.	AR061: 0, AR089: 0 H0519: 1 and H0521: 1.			
		966597	303	1 - 366	627					
149	HTPGQ16	1027781	159	3 - 806	483	His-1 to Lys-6, His-75 to Phe-84, Asp-91 to Phe-96, Pro-99 to Phe-110, Tyr-158 to Trp-164, Pro-169 to Ser-177, Gly-185 to Ala-207.	AR061: 9, AR089: 4 H0624: 1, H0622: 1, H0539: 1 and L0581: 1.			
		909618	304	145 - 843	628	His-62 to Phe-71, Asp-78 to Phe-83,				

150	HOCMS18	1227594	160	1 - 1029	484	Pro-86 to Phe-97, Tyr-145 to Thr-150, Lys-180 to Ala-193.	AR089: 2, AR061: 0 L0777: 14, L0740: 9, H0050: 5, L0599: 5, L0747: 4, L0759: 4, S0040: 3, H0599: 3, H0031: 3, L0770: 3, L0803: 3, L0647: 3, S0328: 3, S3014: 3, S0206: 3, L0756: 3, L0779: 3, L0731: 3, L0758: 3, S0116: 2, S0360: 2, H0619: 2, H0575: 2, H0251: 2, H0545: 2, H0266: 2, H0135: 2, H0040: 2, H0551: 2, H0059: 2, L0764: 2, L0776: 2, L0659: 2, H0144: 2, H0547: 2, S0037: 2, L0744: 2, L0749: 2, H0506: 2, H0295: 1, S0212: 1, S0418: 1, S0007: 1, S0046: 1, H0645: 1, S0222: 1, L0468: 1, H0333: 1,	Ala-1 to Ser-11, Pro-52 to Gly-61, Thr-68 to Gly-103, Lys-114 to Ala-120, Pro-122 to Arg-127, Gly-136 to Thr-147, Asn-150 to Arg-167, Lys-186 to Gln-193, Ser-195 to His-200, Ser-208 to Glu-215, Tyr-234 to Thr-242.			

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151	HE8AM58	1204936	161	1 - 954	485	Gly-1 to Ser-11, Ser-18 to Ala-25, Ser-70 to Cys-77, Asp-89 to His-104.	AR061: 424, AR089: 326 H0370: 1, H0013: 1 and S0330: 1.		
		894346	306	2 - 460	630	Ser-65 to Cys-72, Asp-84 to His-99, Arg-107 to Asn-112.			
152	HUSGZ51	955542	162	3 - 356	486	Ile-45 to Arg-52, Phe-77 to Pro-85.	AR089: 11, AR061: 5 H0556: 10, L0748: 8, H0620: 7, L0747: 7, H0265: 5, L0637: 5, H0013: 4, H0551: 4, L0776: 4, L0663: 4, L0596: 4, H0622: 3, H0617: 3, L0772: 3, L0766: 3, S0126: 3,		

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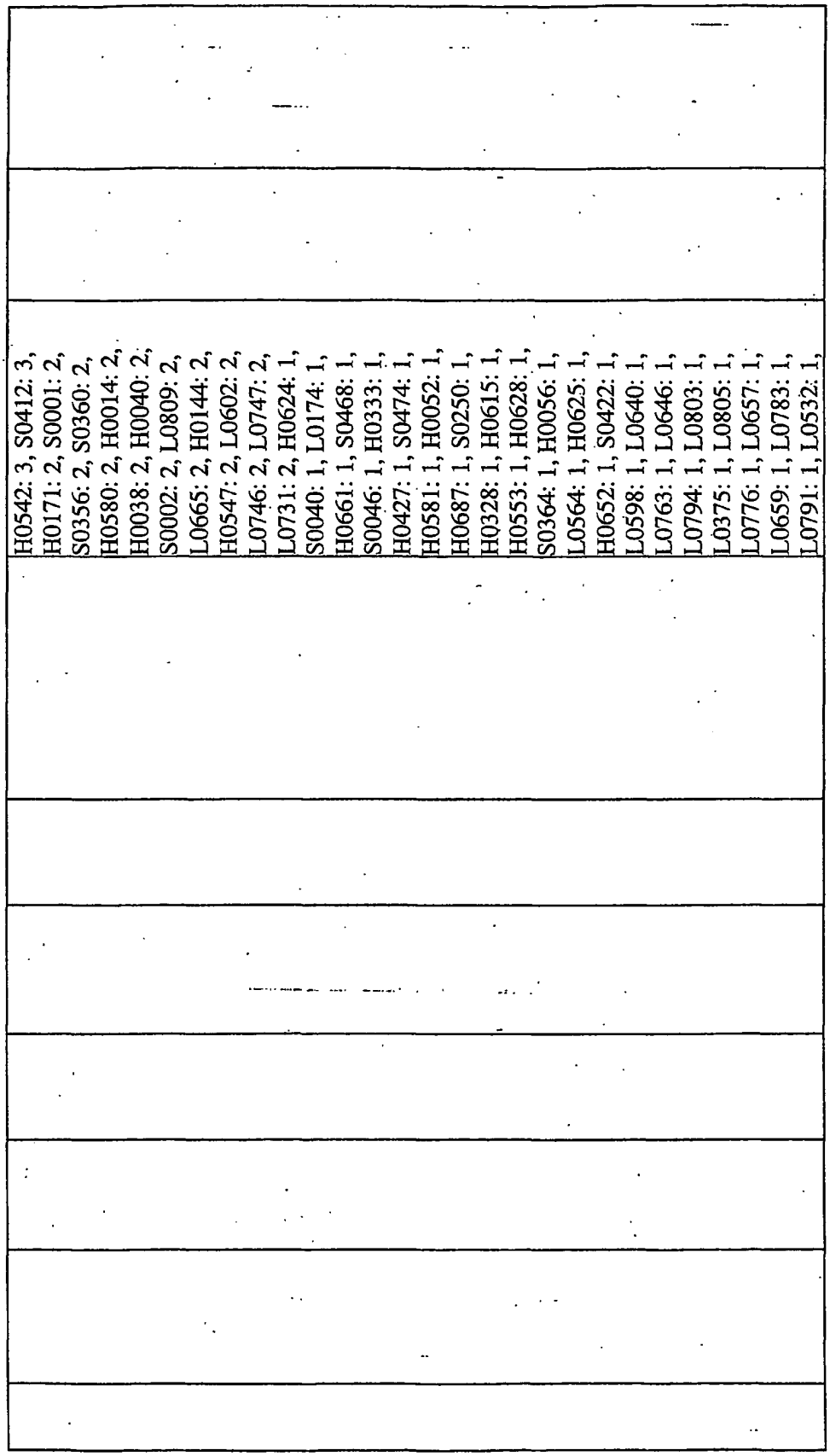
153	HELEQ48	960866	163	48 - 500	487		AR089: 1, AR061: 0 H0424: 5, S0045: 1, H0051: 1, S0051: 1, H0213: 1, H0616: 1, H0079: 1, L0639: 1, L0662: 1, L0794: 1, L0803: 1, L0804: 1, L0774: 1, L0805: 1, L0659: 1, L0789: 1 and L0742: 1.		
154	HOFOE03	1226251	164	2117 - 3	488	Gln-14 to Pro-21, Ala-46 to Trp-51, Ala-79 to Thr-86, Lys-179 to Thr-185, Asn-210 to Gly-216, Asn-243 to Gly-249, Met-278 to Pro-286.	AR089: 1, AR061: 0 H0415: 1, H0575: 1; H0560: 1 and H0561: 1.		
		911616	307	127 - 840	631				
155	HNFFR23	585289	165	3 - 335	489		AR089: 0, AR061: 0 H0271: 1 and S0044: 1.		
156	HOGCC57	1205511	166	95 - 754	490	Ala-15 to Arg-31, Ala-55 to Gly-62, Glu-122 to Gly-128, His-150 to Asn-155, Val-187 to Arg-195.	AR089: 2, AR061: 1 L0748: 2, H0622: 1, H0551: 1, L0774: 1, L0776: 1, H0435: 1 and L0751: 1.		

		911609	308	95 - 754	632	Ala-15 to Arg-31, Ala-55 to Gly-62, Glu-122 to Gly-128, His-150 to Asn-155, Val-187 to Arg-195.			
157	HFOZC96	926685	167	1 - 309	491	Pro-1 to Gly-7, Gln-52 to Cys-61, His-88 to Tyr-93.	AR089: 1, AR061: 1 L0766: 6, L0748: 3, L0779: 3, S0360: 2, H0545: 2, H0494: 2, L0769: 2, L0731: 2, L0759: 2, L0599: 2, H0295: 1, L0622: 1, L0021: 1, H0052: 1, H0546: 1, H0457: 1, H0086: 1, H0123: 1, H0413: 1, L0646: 1, L0768: 1, L0381: 1, L0659: 1, L0783: 1, L0809: 1, L0790: 1, L0666: 1, L0663: 1, H0539: 1, S3012: 1, L0747: 1, S0276: 1, H0543: 1 and H0352: 1.		
158	HOHBK44	823872	168	3 - 527	492	Ser-1 to Arg-6, Arg-37 to Thr-43.	AR089: 1, AR061: 1 L0740: 11, L0662: 4, L0756: 4, L0777: 4, L0758: 4, L0649: 3, L0666: 3, L0748: 3,		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159	HHERB37	708477	169	3 - 320	493	Pro-1 to Pro-8, Phe-12 to Thr-17, Lys-60 to Gly-66, Lys-71 to Gly-77, Pro-88 to Gln-97.	L0663: 1, L0565: 1, H0519: 1, H0670: 1, H0436: 1, H0478: 1, L0749: 1, L0779: 1, L0752: 1, L0755: 1, L0757: 1, H0445: 1, S0011: 1, H0668: 1, H0667: 1, S0276: 1 and S0398: 1.		
160	HEGAW40	710652	170	69 - 686	494	Pro-8 to Trp-15, Gly-42 to Gly-51, Thr-58 to Arg-69.	AR089: 2, AR061: 1 L0438: 4, L0471: 2, L0439: 2, L0731: 2, H0149: 1, S0040: 1, H0438: 1, L0623: 1, H0156: 1, T0010: 1, H0424: 1, L0774: 1, L0657: 1, L0750: 1, L0777: 1, L0592: 1 and H0543: 1.		
161	HDTDQ51	1152264	171	151 - 699	495	Lys-32 to Asp-37, Pro-116 to Glu-132.	AR061: 1, AR089: 0 L0766: 6, L0747: 3, L0803: 2, L0777: 2, H0550: 1, H0013: 1, L0773: 1, L0805: 1, L0809: 1, L0789: 1 and L0740: 1.		
							AR061: 2, AR089: 1 L0766: 3, L0764: 2,		

				823871	309	140 - 598	633	Lys-32 to Asp-37, Pro-116 to Pro-137.	L0771: 2, L0439: 2, L0756: 2, L0731: 2, S0192: 2, S0134: 1, H0415: 1, H0486: 1, H0057: 1, T0006: 1, H0031: 1, L0598: 1, L0800: 1, L0768: 1, L0794: 1, L0774: 1, L0783: 1, L0519: 1, L0663: 1, L0664: 1, L0352: 1, H0522: 1, L0748: 1, L0747: 1 and L0749: 1.		
162	HOHCG42	1152272	172	3 - 488	496	Tyr-8 to Asn-13, Arg-62 to Arg-67, Lys-95 to Thr-102.	AR089: 1, AR061: 1 S0250: 2, H0556: 1 and H0561: 1.				
				887839	310	143 - 409	634	Arg-15 to Arg-27.			
163	HOVCC60	718918	173	2 - 604	497		AR089: 9, AR061: 4 L0439: 21, L0438: 5, L0758: 3, H0520: 2, L0747: 2, L0756: 2, L0777: 2, H0171: 1, S0420: 1, S0007: 1, H0024: 1, H0373: 1, L0163: 1, S0003: 1, H0428: 1, L0762: 1,				

164	HMVAC92	731732	174	2 - 466	498		L0805: 1, L0666: 1, H0547: 1, L0752: 1 and L0753: 1.			
							AR089: 12, AR061: 2	Xp11.4-p11.1		300047, 300062, 300600, 309470, 309500, 309610, 310500, 310600, 310600, 311050, 312060
165	HWGAF89	742053	175	86 - 661	499	Ala-33 to Ser-41, Ser-57 to Asp-65, Asp-77 to Asn-85, Ser-99 to Gln-109.	AR089: 4, AR061: 1 L0439: 10, L0803: 7, L0663: 6, H0423: 5, L0655: 4, L0740: 4, S0222: 3, L0649: 3, L0759: 3, H0553: 2, L0766: 2, L0438: 2, H0520: 2, S0330: 2, L0751: 2, L0746: 2, L0747: 2, H0170: 1, H0686: 1, H0650: 1, H0657: 1, S0116: 1, H0341: 1, S0356: 1, S0408: 1, S0410: 1,			

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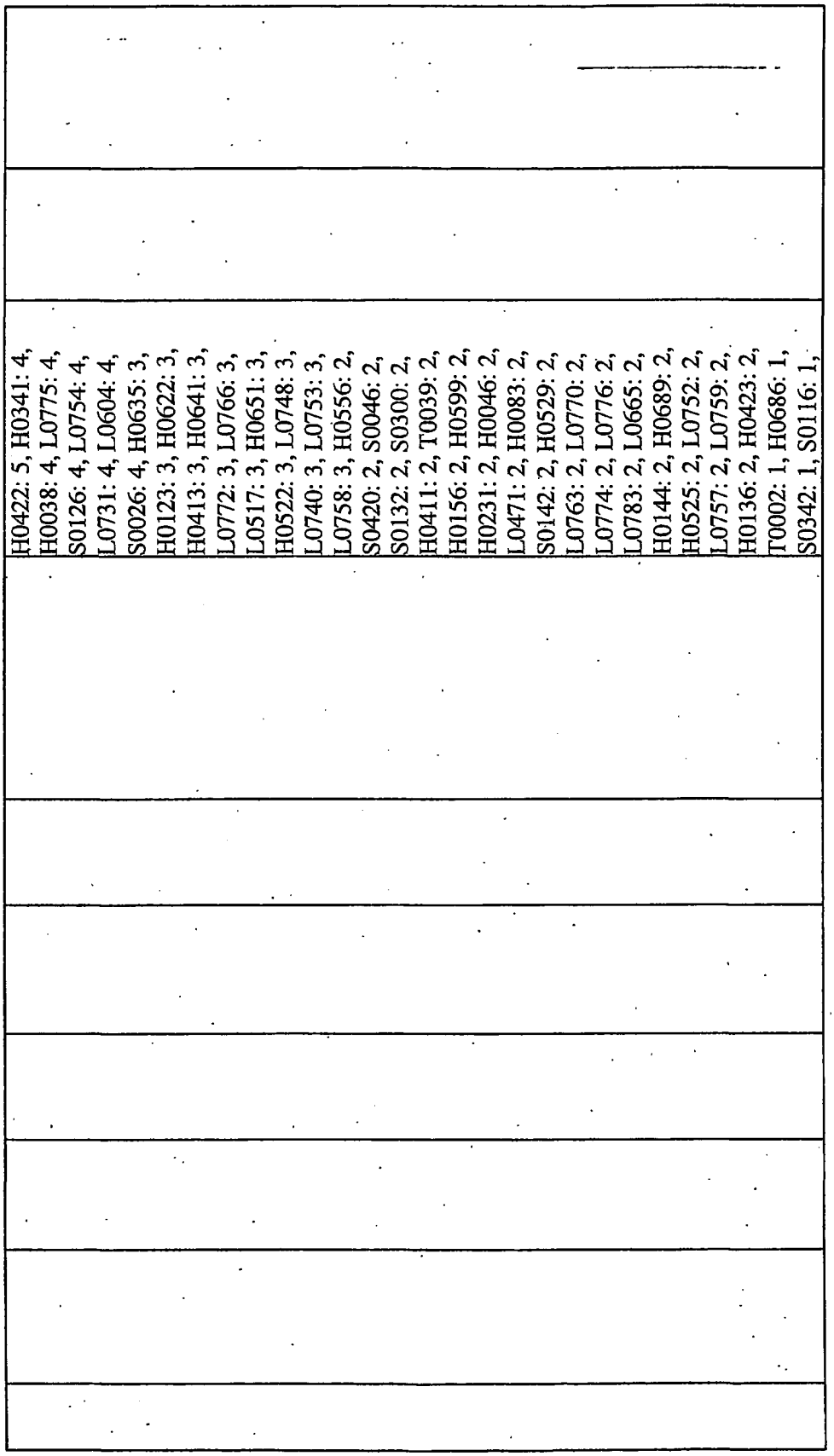
166	HHBEG78	969106	176	73 - 456	500	Ser-73 to His-81, His-83 to Thr-89.	AR089: 1, AR061: 1 S0358: 12, H0659: 8, H0657: 7, H0624: 6, S0360: 6, H0373: 6, L0588: 6, H0543: 6, L0769: 5, L0747: 5,	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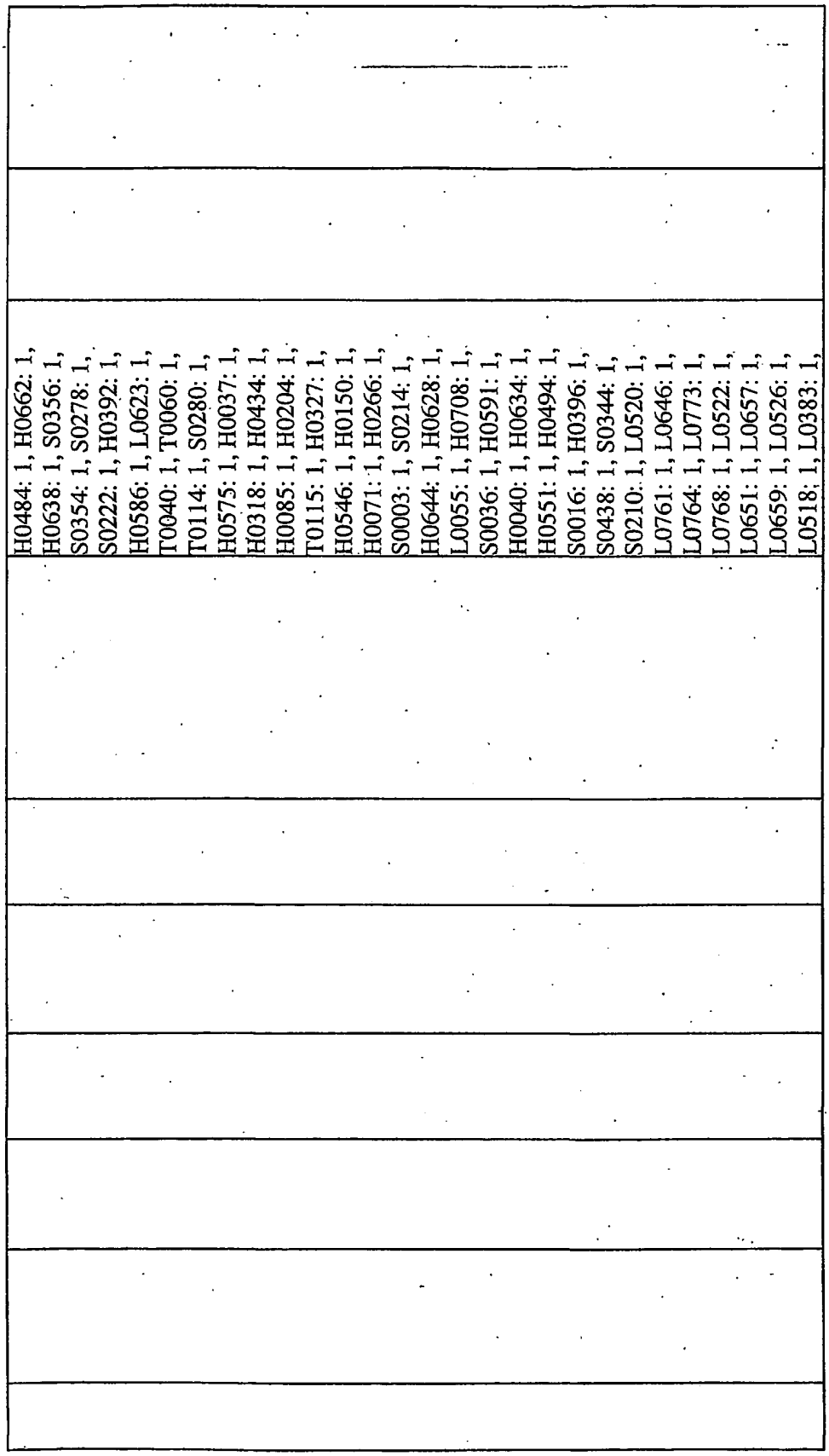
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167	HPMJT61	1152422	177	195 - 515	501	Glu-1 to Ala-7, Pro-9 to Leu-28, Glu-36 to Met-52, Pro-76 to Cys-90, Ser-98 to Pro-107.	AR061: 6, AR089: 3 L0748: 4, L0809: 3, L0439: 3, L0777: 2, L0589: 2, S0278: 1, H0024: 1, H0644: 1, L0791: 1, H0547: 1, L0749: 1 and H0352: 1.		
		950367	311	1 - 585	635	Pro-19 to Ala-25, Ser-62 to Gly-68, Pro-97 to Leu-116, Glu-124 to Met-140, Pro-164 to Lys-181; Ser-186 to His-192.			
168	HKAED89	827573	178	1 - 540	502		AR089: 2, AR061: 1 L0748: 395, H0510:		

		165, H0014: 160, L0581: 160, H0046: 150, H0393: 142, H0144: 116, H0509: 86, H0574: 78, H0355: 31, H0013: 29, L0605: 25, H0331: 22, H0015: 21, H0246: 20, H0087: 20, H0197: 16, L0615: 15, H0357: 14, L0599: 10, H0116: 9, S0376: 8, H0575: 7, H0350: 7, H0199: 7, T0078: 7, L0065: 7, L0747: 7, L0750: 7, H0151: 5, H0351: 5, H0349: 5, H0036: 5, H0596: 5, H0057: 5, H0039: 5, S0438: 5, S0358: 4, H0356: 4, H0617: 4, H0102: 4, S0002: 4, L0775: 4, L0777: 4, L0731: 4, S0436: 4, T0114: 3, H0590: 3, S0052: 3, H0149: 2, H0402: 2, S0356: 2, H0282: 2, H0270: 2, H0250: 2, H0156: 2,				

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				90 - 866			
			179				
		850272					
	HHAMA35						
169							

170	HRADJ08	1179715	180	193 - 1059	504	His-116 to Gly-121, His-220 to Gly-226.	AR089: 4, AR061: 2 L0803: 6, L0742: 5, L0809: 3, L0748: 3, L0749: 3, H0599: 2, L0766: 2, L0666: 2, L0665: 2, L0439: 2, L0756: 2, L0753: 2, L0588: 2, S0282: 1, S0356: 1, S0354: 1, S0358: 1, S0360: 1, S0222: 1, H0643: 1, H0331: 1, T0039: 1, H0013: 1, S0049: 1, H0014: 1, L0163: 1, S0388: 1, S0051: 1, H0622: 1, H0163: 1, H0059: 1, L0435: 1, L0520: 1, L0770: 1, L0761: 1, L0772: 1, L0643: 1, L0764: 1, L0767: 1, L0804: 1, L0775: 1, L0805: 1,	H0593: 1, H0670: 1, H0651: 1, S0176: 1, S0027: 1, L0749: 1, L0750: 1, L0604: 1, S0192: 1, S0194: 1 and S0196: 1.		

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		958556	312	182 - 724	636	His-116 to Gly-121.					
171	HLYAN64	867366	181	603 - 1442	505	Pro-5 to Arg-11, Pro-25 to Gly-30, Leu-200 to Ala-217, Ser-228 to Ser-233, Trp-252 to Ser-259.		AR089: 7, AR061: 5 H0046: 16, L0439: 5, L0493: 4, H0265: 2, L0764: 2, L0741: 2, H0170: 1, L0562: 1, H0675: 1, H0587: 1, H0618: 1, H0009: 1, H0620: 1, H0099: 1, H0039: 1, H0213: 1, H0100: 1, H0561: 1, S0344: 1, L0369: 1, L0768: 1, L0499: 1, L0375: 1, L0513: 1, L0659: 1, L0783: 1, L0382: 1, L0809: 1, L0791: 1, L0666: 1, L0747: 1, L0750: 1, H0445: 1, L0592: 1, H0543: 1 and H0352: 1.	11q23.2	261640, 602574, 602574
172	HTLHP64	883120	182	125 - 445	506	Ile-36 to Arg-41,		AR061: 2, AR089: 1			

					Gly-69 to Lys-82.	L0764: 4, L0777: 4, H0618: 3, H0251: 3, S0358: 2, H0253: 2, H0052: 2, H0617: 2, L0743: 2, H0657: 1, H0255: 1, H0661: 1, H0662: 1, H0402: 1, H0638: 1, S0354: 1, L0622: 1, H0546: 1, S6028: 1, H0213: 1, L0772: 1, L0775: 1, L0657: 1, L0659: 1, L0809: 1, L0666: 1, S0330: 1, S0378: 1, H0696: 1, S0404: 1, H0478: 1, L0744: 1, L0750: 1, L0753: 1, L0731: 1 and H0445: 1.		
173	HNTCI60	890754	183	2 - 808	507	AR089: 1, AR061: 1 L0747: 12, L0766: 10, H0683: 9, L0776: 7, H0521: 6, L0764: 4, L0439: 4, L0750: 4, L0731: 4, H0624: 3, S0222: 3, H0457: 3, H0051: 3, L0770: 3, L0769: 3, L0790: 3, L0666: 3, L0664: 3,		

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174	HUCMU74	899751	184	1 - 705	508	Pro-18 to His-34, Ser-86 to Arg-91, Gln-145 to Thr-150, Thr-165 to Ser-172, Glu-178 to Pro-184.	L0803: 1, L0657: 1, L0659: 1, L0663: 1, S0428: 1, H0701: 1, S0148: 1, L0438: 1, H0520: 1, H0659: 1, H0648: 1, H0672: 1, S0328: 1, S0380: 1, H0627: 1, H0631: 1, S0028: 1, L0744: 1, L0754: 1, L0756: 1, L0779: 1, L0752: 1, S0434: 1, L0605: 1, L0485: 1, H0136: 1, S0192: 1, H0543: 1, H0422: 1 and S0412: 1.	AR089: 6, AR061: 4 S0420: 1			
175	HWWGT02	908017	185	441 - 827	509	Ser-27 to Gln-40, Asp-102 to Lys-109.		AR089: 6, AR061: 4 H0650: 1, H0657: 1, H0271: 1, S0003: 1, L0748: 1 and L0747: 1.			
176	HSKDU47	1154797	186	2 - 580	510	Leu-59 to Trp-65, Trp-91 to Pro-101, Cys-121 to Cys-131.		AR089: 14, AR061: 6 L0649: 2, S0332: 1, S0027: 1, L0593: 1 and H0543: 1.			

		953264	313	3 - 857	637	Leu-56 to Trp-62, Trp-88 to Pro-98, Cys-118 to Cys-128, Lys-207 to Thr-213, Ile-224 to Ser-233, Gly-254 to Ile-261, Gln-268 to Asp-274.			
177	HODFI03	918008	187	551 - 1279	511		AR089: 31, AR061: 4 L0766: 4, L0745: 4, S0222: 3, L0662: 3, L0803: 3, H0013: 2, H0581: 2, H0090: 2, L0774: 2, H0144: 2, L0608: 2, T0002: 1, H0657: 1, H0619: 1, H0411: 1, H0592: 1, H0587: 1, H0486: 1, H0052: 1, T0010: 1, H0375: 1, H0594: 1, S6028: 1, S0250: 1, S0214: 1, H0328: 1, H0615: 1, L0483: 1, L0055: 1, H0124: 1, H0038: 1, H0040: 1, H0487: 1, H0412: 1, T0041: 1, L0646: 1, L0648: 1, L0767: 1, L0649: 1, L0659: 1,		

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178	HWHHR02	919169	188	3 - 671	512		AR061: 6, AR089: 2 L0770: 4, L0771: 4, L0769: 3, L0757: 3, L0766: 2, L0779: 2, L0758: 2, H0170: 1, H0686: 1, H0586: 1, L0637: 1, L0761: 1, L0803: 1, L0774: 1, L0776: 1, L0659: 1, L0809: 1, L0791: 1, H0658: 1, H0696: 1, S3012: 1, S0390: 1, L0747: 1, L0752: 1, L0753: 1, L0759: 1, L0592: 1 and H0543: 1.	7q22	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447
179	HSVBQ03	924850	189	352 - 101	513		AR089: 3, AR061: 3 L0747: 6, L0748: 2, L0755: 2, S0040: 1, H0392: 1, H0587: 1, H0575: 1, H0251: 1,		

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180	HSLCQ10	1153914	190	2 - 352	514	Arg-8 to Thr-13, Gly-58 to Asp-63, Pro-71 to Ala-78, Val-80 to Thr-86.	AR061: 3, AR089: 3 H0521: 3, H0619: 2, L0471: 2, H0341: 1, S0046: 1, H0645: 1, H0587: 1, H0486: 1, H0052: 1, H0457: 1, H0050: 1, H0266: 1, S0003: 1, H0622: 1, L0659: 1, H0520: 1, H0539: 1, S0152: 1, S0028: 1, L0740: 1, L0754: 1, L0592: 1, H0665: 1, H0667: 1 and H0543: 1.		
								963625	314	588 - 1376	638	Thr-48 to His-54,	

181	HKACQ38	975382	191	1 - 1140	515	Thr-62 to Asn-71, Asn-174 to Gly-181.	Pro-1 to Trp-6, Pro-19 to Pro-27, Ala-61 to Asp-70, Ala-93 to Ser-102, Asp-109 to Ser-123, Arg-137 to Thr-154, Pro-163 to Ser-169, Ser-199 to Arg-207, Ser-225 to Gly-239, Gln-255 to Ser-269, Ala-279 to Gly-284, Gln-329 to Cys-338, His-365 to Tyr-370.	AR089: 56, AR061: 23 L0766: 6, L0748: 3, L0779: 3, S0360: 2, H0545: 2, L0769: 2, H0539: 2, L0731: 2, L0759: 2, L0599: 2, H0295: 1, L0622: 1, L0021: 1, H0052: 1, H0546: 1, H0457: 1, H0086: 1, H0123: 1, H0413: 1, H0494: 1, L0646: 1, L0768: 1, L0381: 1, L0659: 1, L0783: 1, L0809: 1, L0790: 1, L0666: 1, L0663: 1, S3012: 1, L0747: 1, S0276: 1, H0543: 1 and H0352: 1.		
		948607	315	39 - 1220	639	Arg-9 to Trp-20, Pro-33 to Pro-41, Ala-75 to Asp-84, Ala-107 to Ser-116, Asp-123 to Ser-137, Arg-151 to Thr-168, Pro-177 to Ser-183, Ser-213 to Arg-221,				

182	HE9GZ52	964579	192	1 - 252	516	Ser-239 to Gly-253, Gln-269 to Ser-283, Ala-293 to Gly-298, Gln-343 to Cys-352, His-379 to Tyr-384.	AR089: 1, AR061: 0 H0013: 1, H0050: 1, S6028: 1 and H0144: 1.		
183	HSYBD55	1197348	193	3 - 446	517	Ser-7 to Arg-12.	AR089: 1, AR061: 1 H0052: 1 and H0551: 1.		
		863287	316	3 - 446	640	Ser-7 to Arg-12.			
184	HTAJM37	1152423	194	3 - 653	518	Lys-52 to Tyr-57, Val-115 to Gly-122, Gln-152 to Pro-159.	AR089: 18, AR061: 11 S0278: 1, H0635: 1, H0038: 1, H0560: 1, H0539: 1, H0521: 1 and L0748: 1.		
		911599	317	119 - 847	641	Gln-9 to Gly-14, Gln-21 to Gln-27, Cys-29 to Gln-38, Pro-52 to Trp-62, Lys-109 to Tyr-114, Val-172 to Gly-179, Gln-209 to Pro-216.			
185	HSDJH63	941120	195	45 - 1250	519	Thr-17 to Lys-23, Lys-93 to Arg-98.	AR089: 17, AR061: 14 H0615: 2, L0766: 2, S0114: 1, H0650: 1,		

								H0657: 1, L0791: 1, H0689: 1, S0152: 1, S0260: 1 and H0445: 1.		
186	HNNAG23	1137691	196	15 - 509	520			AR089: 1, AR061: 0 H0677: 19, H0255: 6, H0318: 5, H0264: 3, L0766: 3, H0656: 2, H0620: 2, L0655: 2, L0659: 2, H0583: 1, H0650: 1, S0222: 1, H0441: 1, H0486: 1, T0082: 1, H0421: 1, H0354: 1, H0688: 1, L0768: 1, L0794: 1, L0809: 1, L0665: 1, H0134: 1 and H0445: 1.		
		967549	318	66 - 716	642	Arg-12 to Arg-21, Pro-35 to Pro-41, Gly-46 to Cys-52, Thr-75 to Gly-84, Thr-87 to Ser-93.				
187	HYAAL21	943135	197	212 - 1159	521	Leu-9 to Leu-14, Pro-22 to Ser-27, Val-132 to Trp-138.		AR089: 20, AR061: 5 H0038: 2, H0583: 1, H0125: 1, H0046: 1, H0529: 1, S0216: 1, H0144: 1, H0539: 1 and S0027: 1.		
188	HPBCF69	946469	198	212 - 688	522			AR061: 8, AR089: 3		

189	HWDAE40	947007	199	157 - 2022	523	Asn-118 to Leu-123, Gly-212 to Thr-217, Arg-265 to Phe-272, Asn-286 to Asp-294, Ala-356 to Asn-364, Cys-385 to Arg-392, Val-437 to Glu-450, Glu-497 to Leu-502, Lys-553 to Tyr-569.	T0006: 1 AR061: 0, AR089: 0 L0748: 10, L0749: 7, L0439: 6, L0731: 6, L0750: 5, S0222: 4, L0756: 4, L0758: 4, L0598: 3, L0754: 3, L0745: 3, L0747: 3, L0777: 3, L0752: 3, L0755: 3, H0170: 2, H0171: 2, H0455: 2, S6028: 2, T0069: 2, L0662: 2, L0776: 2, L0665: 2, H0144: 2, L0438: 2, L0744: 2, L0759: 2, L0485: 2, H0624: 1, S6024: 1, S0400: 1, H0255: 1, L0005: 1, S0358: 1, S0045: 1, H0619: 1, L0717: 1, H0441: 1, H0600: 1, H0486: 1, H0427: 1, H0599: 1, H0590: 1, S0010: 1, S0346: 1, H0581: 1, H0596: 1, H0327: 1, L0157: 1, L0471: 1, H0355: 1, H0267: 1,		

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190	HUVHH77	948377	200	84 - 1019	524	Trp-4 to Pro-9, Phe-36 to Ser-47.	AR061: 4, AR089: 2 L0439: 6, L0777: 6, L0748: 2, L0747: 2, H0171: 1, H0013: 1, H0081: 1, S0250: 1, H0623: 1, S0426: 1, L0521: 1 and L0759: 1.		

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191	HTLIT03	966870	201	2 - 823	525	His-1 to Asp-7, Asp-56 to Tyr-64.	AR061: 11, AR089: 5 H0457: 10, H0253: 7, H0618: 5, L0768: 2, L0748: 2, H0657: 1, S0300: 1, H0550: 1, L0021: 1, H0581: 1, H0617: 1, H0606: 1, H0316: 1, H0038: 1, H0616: 1, H0334: 1, L0761: 1, L0764: 1, L0774: 1, L0659: 1, H0519: 1, H0704: 1, L0755: 1, L0758: 1, L0361: 1 and H0543: 1.		
192	HUJDA09	951526	202	3 - 779	526	Pro-1 to Asp-23, Ile-55 to Gly-81, Glu-150 to Glu-155, Gly-194 to Gly-200.	AR089: 13, AR061: 3 H0650: 1 and H0292: 1.	Xp11.23	300047, 300071, 300110, 300600, 301000, 301000, 301830, 309470, 309500, 309610, 309850, 311050, 312060

193	HTEPU67	1152262	203	2 - 1342	527	Gly-1 to Arg-7, Ala-26 to Ala-33, Gly-86 to His-91, Ser-153 to Ser-167, Pro-182 to Ser-198, Asn-200 to Ser-214, Glu-234 to His-239, Leu-241 to Arg-247, Ser-259 to Phe-271, Leu-280 to Lys-296, Ser-299 to Gln-311, Ala-335 to Ala-342, Glu-356 to Gln-362, Gln-369 to Ile-379, Arg-401 to His-408, Tyr-415 to Thr-420, Ser-435 to Pro-446.	AR061: 4, AR089: 3 L0743: 2, L0779: 2, S0046: 1, H0457: 1, L0471: 1, H0616: 1, L0598: 1, L0794: 1, L0659: 1, L0809: 1, H0547: 1, L0777: 1, S0026: 1 and S0398: 1.		
		948288	319	1 - 546	643	Ala-58 to Ala-65.				
194	HULFJ52	952928	204	2 - 559	528	Arg-1 to Ala-15, Arg-17 to Gly-22, Asp-121 to Leu-128, Asp-180 to Tyr-185.	AR089: 8, AR061: 5 L0779: 10, L0731: 9, L0775: 7, L0740: 6, H0666: 5, H0341: 4, L0769: 4, L0766: 4, L0758: 4, S0278: 3, S0222: 3, H0370: 3, S0003: 3, S0144: 3, L0768: 3, L0774: 3, H0659: 3, S0380: 3,		

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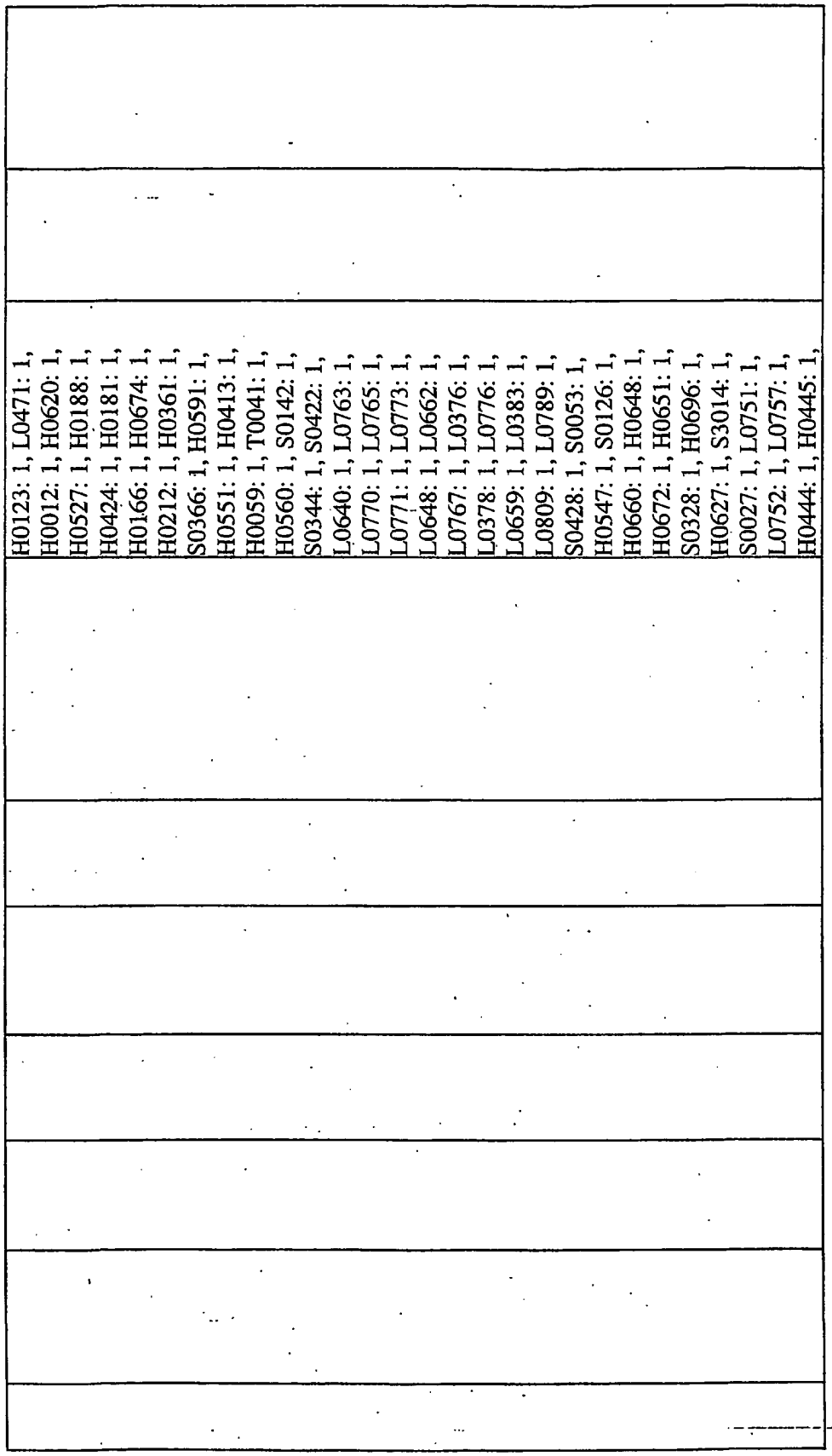
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195	HTEPV02	1152263	205	2 - 586	529	Gly-1 to Ala-6, Ser-19 to Ser-27, Phe-31 to Leu-55, Glu-72 to His-79, Asn-120 to Gly-126, Arg-158 to Arg-163.	L0594: 1, S0026: 1, H0542: 1, H0422: 1 and S0424: 1.	
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		917406	320	1 - 471	644	Ser-9 to Ser-17, Phe-21 to Leu-45.		
196	HTHBT91	954877	206	257 - 433	530		AR061: 5, AR089: 5 L0766: 9, H0657: 4, L0520: 4, H0170: 3, S0360: 3, H0040: 3, L0794: 3, H0144: 3, S0354: 2, T0039: 2, H0412: 2, H0494: 2, L0764: 2, S0126: 2, L0748: 2, L0752: 2, L0755: 2, S0026: 2, H0422: 2, H0556: 1, S0218: 1, H0583: 1, H0656: 1, S0116: 1, H0341: 1, H0669: 1, H0661: 1, S0418: 1, L0005: 1, S0045: 1, S0132: 1, H0642: 1,	

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197	HFVIH16	1164631	207	64 - 1440	531	Arg-31 to Val-38, Arg-80 to Pro-90, Asn-183 to Val-190, Val-318 to Leu-327, Leu-329 to Leu-354, Gln-357 to Glu-367, Leu-373 to Glu-380, Arg-391 to Gly-396, Ser-444 to Ser-457.	AR061: 2, AR089: 2 H0393: 1, N0006: 1 and H0690: 1.		
		813110	322	64 - 390	646	Arg-31 to Val-38, Arg-80 to Pro-90.			
198	HTJAB35	491273	208	519 - 313	532		AR089: 14, AR061: 3 H0063: 2, H0487: 1 and H0445: 1.		
		853995	323	358 - 185	647				
		880424	324	239 - 457	648				
199	HRABP94	970481	209	219 - 1433	533	Met-1 to Gly-17, Pro-22 to Gly-30, Gly-72 to His-82, Leu-89 to Lys-95.	AR089: 5, AR061: 2 S0126: 3, H0624: 1, H0341: 1, S0282: 1, H0550: 1, H0253: 1, H0031: 1, T0042: 1, H0555: 1, L0740: 1 and L0596: 1.		
200	HWAGC08	958139	210	1 - 432	534	Asn-31 to Leu-38, Cys-53 to Cys-64, Gly-139 to Cys-144.	AR089: 1, AR061: 1 L0596: 4, L0758: 2, H0392: 1, S0010: 1, H0581: 1, H0038: 1,		

201	HRDET35	945350	211	12 - 998	535			L0761: 1, L0521: 1, L0766: 1 and H0696: 1.		
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202	HGBIA24	1153890	212	1 - 714	536		Gly-1 to Pro-11, Gln-71 to Thr-77, Arg-187 to Lys-193,	AR061: 5, AR089: 2 L0662: 4, L0756: 4, L0777: 4, L0758: 4,		

Arg-204 to Ser-209, Asp-228 to Tyr-238.					L0649: 3, L0666: 3, S0412: 3, H0171: 2, S0001: 2, S0356: 2, S0360: 2, H0580: 2, H0014: 2, H0038: 2, H0040: 2, L0809: 2, L0665: 2, H0144: 2, H0547: 2, L0602: 2, L0740: 2, L0746: 2, L0747: 2, L0731: 2, H0542: 2, H0624: 1, L0174: 1, H0661: 1, S0046: 1, H0333: 1, H0427: 1, H0581: 1, H0052: 1, H0687: 1, S0250: 1, H0328: 1, H0615: 1, H0553: 1, H0628: 1, S0364: 1, H0056: 1, L0564: 1, H0625: 1, H0652: 1, S0422: 1, S0002: 1, L0598: 1, L0640: 1, L0763: 1, L0646: 1, L0794: 1, L0803: 1, L0375: 1, L0805: 1, L0776: 1, L0657: 1, L0659: 1, L0783: 1, L0791: 1, L0532: 1,

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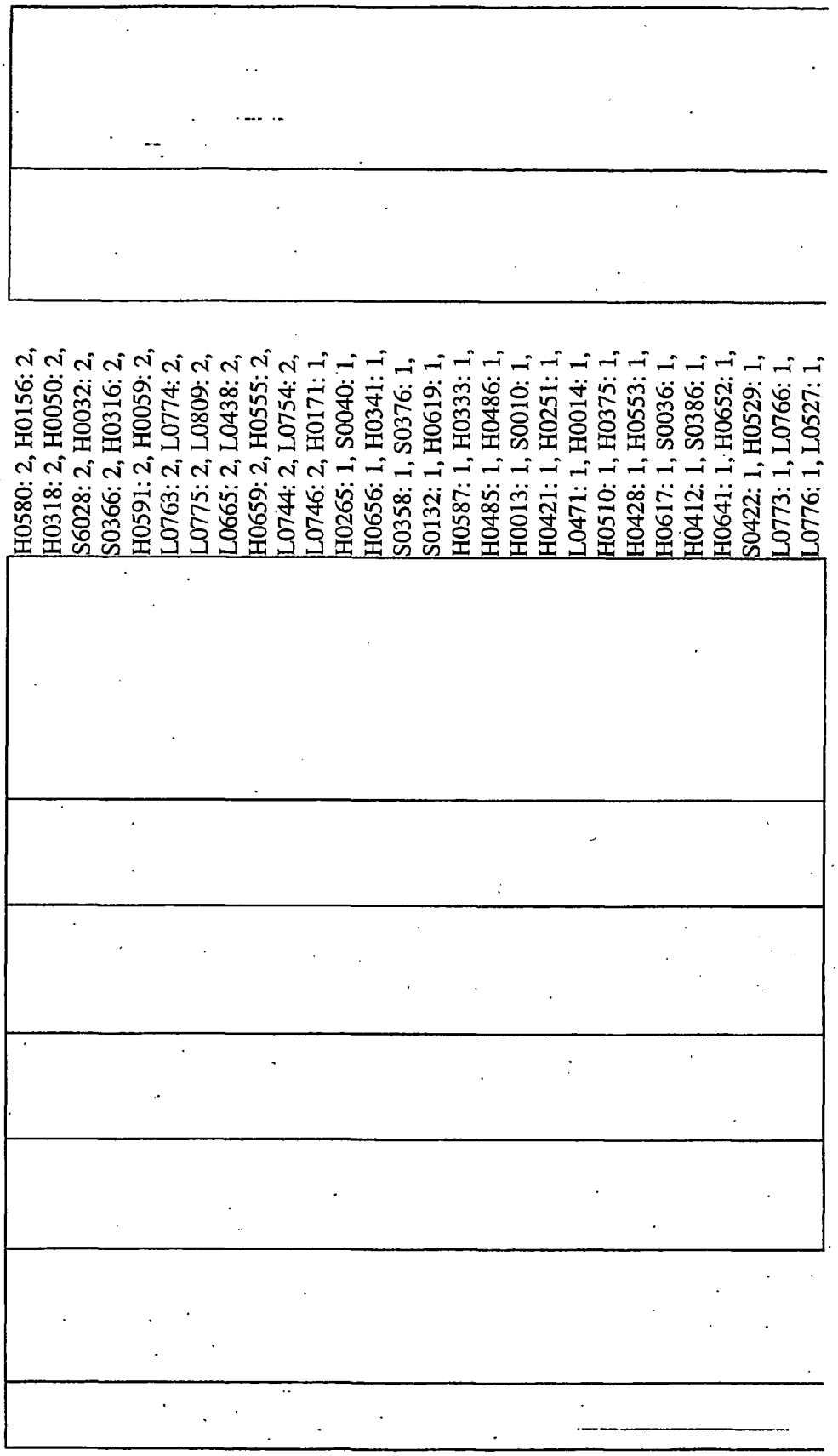
		661111	325	1 - 159	649	Gly-1 to Pro-11, Ser-39 to Thr-53.				
203	HTTHF21	921596	213	186 - 461	537	Met-77 to Asn-92.		AR061: 2, AR089: 0 H0634: 2, S0049: 1 and L0749: 1.		
204	HWHJZ40	964153	214	93 - 1172	538	Gly-12 to Gly-20, Ser-86 to Glu-94, Pro-103 to Pro-110.		AR089: 1, AR061: 0 H0550: 9, H0651: 6, S0358: 5, L0659: 5, H0549: 3, H0586: 3, L0662: 3, L0756: 3, L0777: 3, H0575: 2, L0794: 2, L0649: 2, L0744: 2, L0758: 2, H0662: 1, H0587: 1, H0050: 1, H0018: 1, H0200: 1, H0188: 1, H0687: 1, H0644: 1, H0628: 1, H0163: 1, H0100: 1, L0770: 1, L0809: 1, L0788: 1, L0663: 1, H0696: 1,		

205	HJMBN52	966226	215	3 - 611	539	Thr-3 to Gln-9, Phe-36 to Ala-41, His-52 to Ala-63, Ala-81 to Ser-100, Pro-122 to Ser-134.	S0390: 1, S0028: 1 and L0749: 1.	AR061: 1, AR089: 1 H0402: 2, H0617: 2, L0766: 2, L0659: 2, H0624: 1, H0341: 1, S0212: 1, S0356: 1, S0046: 1, H0370: 1, H0427: 1, H0545: 1, L0769: 1, L0764: 1, L0794: 1, L0651: 1, L0809: 1, L0789: 1, L0438: 1, H0658: 1, H0539: 1, L0439: 1, L0758: 1 and H0445: 1.		
206	HUFCN47	1197927	216	684 - 1490	540	Gly-58 to Cys-64, Lys-74 to Gln-81, Thr-90 to Asp-99, Met-113 to Ser-118, Met-144 to Gln-150, Gln-166 to Gly-173, Thr-180 to Leu-187, Ser-246 to Asp-256.		AR089: 10, AR061: 0 L0803: 12, L0749: 8, L0747: 6, L0755: 6, L0758: 6, L0748: 5, L0439: 5, L0731: 5, L0759: 5, L0662: 4, L0659: 4, L0740: 4, H0052: 3, H0090: 3, H0040: 3, L0666: 3, H0547: 3, S0330: 3, H0521: 3, L0779: 3, L0608: 3, S0276: 3, S0356: 2, S0360: 2,		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			910435	326	1 - 549	650	Ser-12 to Arg-23, Arg-56 to Asp-62.	L0789: 1, L0790: 1, L0663: 1, L0664: 1, H0144: 1, H0682: 1, H0670: 1, H0672: 1, S0328: 1, H0539: 1, S0152: 1, H0522: 1, S0146: 1, S0404: 1, L0356: 1, H0478: 1, L0750: 1, L0752: 1, L0581: 1, L0697: 1, S0446: 1 and H0506: 1.	
207	HHEUC31	1091624	217	3 - 677	541	Glu-26 to Pro-35, Glu-56 to Ser-62, Gln-67 to Val-73, Ser-77 to Thr-82, Ala-90 to Val-104, Thr-126 to Glu-134, Pro-205 to Pro-211.	AR089: 4, AR061: 2 H0543: 2 and L0596: 1.		
		795268	327	3 - 677	651	Glu-26 to Pro-35, Glu-56 to Ser-62, Gln-67 to Val-73, Ser-77 to Thr-82, Ala-90 to Val-104, Thr-126 to Glu-134, Pro-205 to Pro-211.			
208	HUSAL47	1197928	218	45 - 1601	542	Ala-38 to Thr-45,	AR089: 251, AR061:		

						Ser-70 to Asp-77, Ser-85 to Asp-90, Asp-139 to Gly-145, Ile-207 to Asp-213, Arg-229 to Met-234, Gly-259 to Ser-264, Ile-281 to Ser-288, Asp-337 to Leu-343, Gln-369 to Ile-376, Gly-429 to Ser-440, Gln-448 to Val-456, Gln-461 to Thr-474.	130 L0766: 16, L0749: 13, L0748: 12, L0777: 9, L0740: 6, H0341: 3, H0144: 3, H0268: 2, L0779: 2, L0780: 2, H0624: 1, S0430: 1, H0661: 1, S0420: 1, S0045: 1, S0046: 1, S0222: 1, H0013: 1, H0544: 1, L0157: 1, H0320: 1, H0428: 1, H0040: 1, H0551: 1, H0412: 1, H0623: 1, L0564: 1, H0560: 1, H0646: 1, L0520: 1, L0769: 1, L0772: 1, L0364: 1, L0803: 1, L0650: 1, L0378: 1, L0791: 1, L0666: 1, H0519: 1, H0539: 1, S0152: 1, H0521: 1, S0044: 1, H0436: 1, L0754: 1, L0747: 1, L0750: 1, L0731: 1, L0758: 1, L0589: 1, L0608: 1, L0366: 1, S0192: 1 and H0543: 1.		

		911607	328	18 - 644	652	Ala-38 to Thr-45, Ser-70 to Asp-77, Ser-85 to Asp-90, Asp-139 to Gly-145, Arg-189 to Asp-196.			
209	HHFGD38	1153892	219	159 - 683	543	Pro-10 to Trp-21, Ala-70 to Thr-79, Leu-105 to Arg-111.	AR061: 8, AR089: 4 L0759: 3, S0152: 2, L0749: 2, H0441: 1, H0013: 1, H0427: 1, H0156: 1, H0318: 1, H0597: 1, H0050: 1, S0386: 1, H0538: 1, L0803: 1 and L0809: 1.		
		766126	329	159 - 563	653				
210	HVAOG11	1152275	220	161 - 886	544	Asn-16 to Ser-23, Lys-53 to Val-61, Leu-77 to Asp-89, Leu-116 to Ala-121, Glu-152 to Lys-168, Arg-178 to Lys-183, Asp-196 to Glu-203, Glu-220 to Ser-233.	AR089: 2, AR061: 1 H0014: 1, H0039: 1, S0380: 1 and L0740: 1.		
		966135	330	226 - 861	654	Asn-16 to Ser-23, Lys-53 to Asp-60.			
211	HUVDR03	974684	221	1 - 780	545	Leu-27 to Pro-34, Pro-40 to Lys-51, Asn-85 to Phe-90, Arg-102 to Leu-140,	AR089: 5, AR061: 3 L0747: 12, L0766: 10, H0683: 9, L0776: 7, H0521: 6, L0764: 4,		

L0439: 4, L0731: 4, H0624: 3, S0222: 3, H0457: 3, H0051: 3, L0770: 3, L0769: 3, L0790: 3, L0666: 3, L0664: 3, H0547: 3, L0750: 3, L0757: 3, L0759: 3, H0050: 2, H0056: 2, S0210: 2, L0662: 2, L0774: 2, L0519: 2, L0665: 2, H0519: 2, L0748: 2, L0751: 2, S0242: 2, H0556: 1, H0657: 1, H0341: 1, H0484: 1, H0125: 1, S0418: 1, S0354: 1, S0300: 1, S0278: 1, H0370: 1, H0392: 1, H0438: 1, H0600: 1, H0592: 1, T0039: 1, H0250: 1, H0427: 1, H0042: 1, H0575: 1, H0004: 1, H0581: 1, H0421: 1, H0012: 1, H0083: 1, H0408: 1, H0355: 1, H0266: 1, H0271: 1, H0622: 1, H0169: 1,	Gly-145 to Asp-191, Glu-219 to His-227.						

212	HUDAE29	689811	222	58 - 288	546		H0135: 1, H0264: 1, H0272: 1, H0488: 1, H0412: 1, H0623: 1, H0059: 1, H0625: 1, H0641: 1, S0426: 1, L0761: 1, L0646: 1, L0773: 1, L0803: 1, L0657: 1, L0659: 1, L0663: 1, S0428: 1, H0701: 1, S0148: 1, L0438: 1, H0520: 1, H0659: 1, H0648: 1, H0672: 1, S0328: 1, S0380: 1, H0627: 1, H0631: 1, S0028: 1, L0744: 1, L0754: 1, L0756: 1, L0779: 1, L0752: 1, S0434: 1, L0605: 1, L0485: 1, H0136: 1, S0192: 1, H0543: 1, H0422: 1 and S0412: 1.	AR089: 13, AR061: 4 L0750: 2, H0370: 1, H0494: 1 and S0042: 1.		
213	HIBCJ89	954681	223	1968 - 229	547	His-3 to Leu-15, Tyr-28 to Ala-34, Gly-52 to Glu-57,		AR061: 1, AR089: 1 S0048: 1 and T0010: 1.			

		963279	331	367 - 1713	655	Ser-123 to Gly-136.					
214	HIBEG40	504158	224	29 - 403	548	Phe-15 to Glu-24.	AR089: 1, AR061: 1 L0439: 4, T0010: 2 and H0038: 1.				
215	HWBEG33	1195806	225	3 - 1784	549	Pro-26 to Ala-38, Lys-85 to Gly-97, Tyr-120 to Glu-131, Asp-158 to Leu-168, Asn-187 to Gly-197, Ser-204 to Asp-209.	AR089: 14, AR061: 6 H0693: 44, L0604: 5, S0366: 4, L0805: 4, H0637: 3, L0766: 3, H0672: 3, H0549: 2, H0271: 2, L0777: 2, H0661: 1, H0580: 1, H0173: 1, H0620: 1, H0428: 1, S0364: 1, L0641: 1, L0644: 1, L0655: 1, L0809: 1, L0791: 1, L0666: 1, L0663: 1, T0068: 1, H0576: 1, L0780: 1, L0731: 1, L0584: 1 and H0543: 1.				
		702070	332	103 - 591	656	Lys-51 to Gly-63, Tyr-86 to Glu-97.					
216	HWHKD22	1150878	226	3 - 317	550	Thr-1 to Arg-7, Asn-34 to Gly-41, Thr-67 to Asn-75.	AR089: 14, AR061: 8 L0766: 3, L0805: 3, L0659: 3, L0744: 3, L0794: 2, L0776: 2, L0665: 2, H0648: 2,				

							H0305: 1, H0586: 1, H0599: 1, H0428: 1, H0551: 1, L0763: 1, L0637: 1, L0662: 1, L0768: 1, L0803: 1, L0804: 1, L0806: 1, L0655: 1, L0661: 1, L0787: 1, S0374: 1, H0520: 1, L0740: 1, L0750: 1, L0756: 1, L0777: 1, L0752: 1, L0759: 1 and L0592: 1.		
		963626	333	152 - 508	657	Asn-48 to Gly-55, Thr-81 to Asn-89.			
217	HSLFO41	765497	227	1 - 282	551		AR089: 1, AR061: 0 S0052: 1 and S0028: 1.		
218	HE9SE46	944511	228	1 - 1083	552	Ser-40 to Tyr-45, Ala-61 to Pro-71, Gly-92 to Asp-98, Ala-145 to Asp-151, Pro-197 to Cys-205, Leu-224 to Gly-235, Glu-241 to Ala-254, Ser-256 to Asn-262, Asp-279 to Glu-290, Ser-296 to Gly-303, Lys-340 to Arg-345, Ile-347 to Tyr-354.	AR061: 1, AR089: 1 L0776: 20, L0777: 9, L0439: 6, L0438: 4, L0752: 4, L0591: 4, H0013: 3, H0052: 2, H0024: 2, L0415: 1, S0212: 1, S0360: 1, H0586: 1, H0596: 1, H0050: 1, S0050: 1, H0373: 1, S0051: 1, S6028: 1, H0188: 1, S0386: 1, S0448: 1,		

								S0306: 1, L0369: 1, L0774: 1, L0775: 1, L0805: 1, H0144: 1, T0068: 1, S0330: 1, L0745: 1, L0750: 1, L0779: 1, L0755: 1, L0731: 1, S0260: 1, L0596: 1, L0608: 1 and H0665: 1.		
219	HTLDW37	864276	229	216 - 836	553		Thr-1 to Leu-7.	AR089: 18, AR061: 18 H0618: 1, H0253: 1, H0012: 1, H0620: 1, H0181: 1 and H0617: 1.		
220	HWAFG54	1227138	230	17 - 2389	554			AR089: 1, AR061: 1		
		1056330	334	144 - 2336	658		Met-1 to Lys-11, Asp-96 to Ile-104, Asn-127 to Ser-140, Gln-185 to Arg-190, Lys-221 to Ser-231, Ala-254 to Val-262, His-295 to Asp-300, Leu-304 to Ser-323, Ser-327 to Gln-333, Ala-345 to Ser-354, Ala-370 to Ser-384, Thr-396 to Gly-402, Leu-413 to Pro-423,			

221	HKAFS73	810433	231	3 - 410	555	Gly-432 to Val-438, Ser-478 to Phe-485, Arg-487 to Lys-506, Ser-528 to Ser-547, Asn-557 to Ala-566, Asp-586 to Glu-597, Glu-644 to Pro-656, Leu-663 to Arg-671, Ser-700 to Asp-707.		AR089: 31, AR061: 25			
222	HTXJD74	921175	232	3 - 752	556			AR061: 7, AR089: 4 S0116: 2, H0510: 2, H0144: 2, H0521: 2, L0748: 2, H0556: 1, T0049: 1, H0580: 1, H0393: 1, H0587: 1, H0051: 1, H0375: 1, H0622: 1, H0488: 1, H0646: 1, S0002: 1, L0752: 1 and L0731: 1.			
223	HSIGQ50	932448	233	1 - 1302	557	Arg-50 to Gln-56, Gly-109 to Glu-119, Gln-131 to Asp-137, Gly-149 to Gly-159, Leu-184 to Glu-218, Val-239 to Ile-245.		AR061: 1, AR089: 1 H0457: 8, H0255: 6, L0743: 4, H0650: 2, S0354: 2, H0581: 2, L0747: 2, H0341: 1, S0376: 1, H0580: 1, H0069: 1, H0042: 1,	16q22.1		103850, 114835, 116800, 140100, 140100, 192090, 192090,

							H0036: 1, H0590: 1, H0251: 1, H0085: 1, H0123: 1, H0687: 1, H0213: 1, H0135: 1, H0040: 1, H0646: 1, S0002: 1, H0593: 1, H0555: 1, L0748: 1, L0731: 1, L0758: 1, L0596: 1, H0543: 1 and H0506: 1.		192090, 192090, 245900, 245900, 276600, 600223
224	HWWDY45	932607	234	3 - 647	558	Gly-40 to Gly-46, Gln-60 to Arg-69, Lys-84 to Trp-91, Leu-112 to Arg-118.	AR089: 1, AR061: 1 H0657: 1, S0376: 1, H0123: 1, H0428: 1, L0646: 1, L0662: 1, L0803: 1, L0659: 1, L0790: 1, L0791: 1, H0660: 1 and L0759: 1.		
225	HNSMB24	971537	235	3 - 677	559	Ser-15 to Tyr-24, Met-47 to Tyr-56, Gly-127 to Ser-133.	AR089: 34, AR061: 19 L0664: 2, H0483: 1, S0376: 1, L0762: 1, L0638: 1, L0771: 1, L0657: 1, L0783: 1, L0665: 1, H0658: 1, H0670: 1 and L0779: 1.		

226	HWLOU63	946862	236	691 - 662	560		AR089: 3, AR061: 2 L0774: 3, L0771: 2, L0766: 2, L0779: 2, S0376: 1, L0646: 1, L0764: 1, L0666: 1, L0748: 1, L0731: 1, L0593: 1 and H0423: 1.	6	

[35] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

[36] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[37] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[38] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[39] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ^{33}P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[40] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more

sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[41] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[42] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID NO:Z	SEQ ID NO:X	CONTIG ID:	BAC ID: A	SEQ ID NO:B	EXON From-To
HE2KJ64	12	906019	AC020570	659	1-67
					406-542
					1507-1624
					2333-2429
					4080-4222
					4398-4455
					4561-4630
					4836-4971
					7386-7427
					7521-7596
HE2KJ64	12	906019	AC020570	660	1-247
HLICC37	14	856958	AL365356	661	1-195
					1135-2232
					2239-3110
HLICC37	14	856958	AL365356	662	1-173
HLICC37	14	856958	AL365356	663	1-141
HLTER04	23	590990	AC018845	664	1-273
					320-800
					866-1324
					1551-2419
					3945-4348
					5055-5373
					5597-5685
					6123-6519
					7020-7482
					7751-7856
					8955-9162
					9398-9496
					10809-11159
					13498-13544
					13809-14276
					14343-14490
					14632-14762
					16544-18402
HLTER04	23	590990	AC007338	665	1-273
					320-801
					867-1325
					1552-2420

					3946-4349 5056-5374 5598-5686 6124-6520 7021-7483 7752-7857 8956-9163 9399-9497 10810-11160 13499-13545 13810-14277 14344-14491 14633-14763 16545-18403
HLTER04	23	590990	AC018845	666	1-249
HLTER04	23	590990	AC007338	667	1-249
H2MBY83	25	752124	AC017104	668	1-540
H2MBY83	25	752124	AC017104	669	1-548
HMZAD58	27	975304	AC078916	670	1-364
HMZAD58	27	975304	AC022305	671	1-686
HMZAD58	27	975304	AC002518	672	1-247
HMZAD58	27	975304	AC072032	673	1-364
HMZAD58	27	975304	AC078916	674	1-288
HMZAD58	27	975304	AC072032	675	1-288
HCHNH17	28	975378	AC026236	676	1-141
HBIMF04	36	951601	AL022328	677	1-103 1215-1770 2471-2545 3028-3108 3680-3960 4352-4494 4925-5476 6623-6828 6888-9053 9409-10241
HBIMF04	36	951601	AL022328	678	1-333
HBIMF04	36	951601	AL022328	679	1-186 376-570 1511-2312 2355-2630 2996-3446

					3617-4004 4225-5042 5275-5664 5695-5783 6915-7130 7265-7787 8377-9065 9159-9294 9608-9952 10071-10419 11431-11799 12322-12621 12641-12911 14491-14580 14653-14848 15670-15856 15949-16109 16183-16596
HOCQD08	39	972981	AC018568	680	1-1718
HOCQD08	39	972981	AC018568	681	1-425
HE8DL23	43	693641	AL135999	682	1-63 405-942 1196-1502 2152-6417 6659-6755 7033-7385 7481-7535 7647-8163 8230-8492 8590-9909 10114-10360 10420-10783 10970-11960 12018-13492 14130-14528 14563-15789
HE8DL23	43	693641	AL135999	683	1-410
HAJBU67	55	856922	AC008910	684	1-1685 1960-2928
HAJBU67	55	856922	AC026230	685	1-1686 1961-2933

HAJBU67	55	856922	AC008910	686	1-326
HAJBU67	55	856922	AC026230	687	1-91
HAJBU67	55	856922	AC026230	688	1-325
HCEMY90	68	932927	AC024242	689	1-274 1243-1357 1994-2270
HCEMY90	68	932927	AF214633	690	1-274 1243-1357 1994-2270
HCEMY90	68	932927	AC024242	691	1-232
HCEMY90	68	932927	AF214633	692	1-130
HHFLF63	69	933854	AC023295	693	1-75 1512-1564
HDTDG41	72	942490	AL137848	694	1-175 2422-2550 3441-3583 4018-4129 8219-8689 9767-9876 11592-11892 14228-14324 15025-15162 16319-16590 17309-18595
HDTDG41	72	942490	AL137848	695	1-196
HFEBN52	82	810429	AL136001	696	1-61 290-371 654-779 2128-2223 2337-2372 2507-2674 3747-4249 4554-4644 5223-5557 5604-5916 6827-6930 6949-7329 7852-8047
HFEBN52	82	810429	AL359399	697	1-61 290-371 654-779

					2128-2223 2337-2372 2507-2674 3747-4249 4554-4644 5221-5555 5602-5914 6825-6928 6947-7327 7850-8045
HFEBN52	82	810429	AL136001	698	1-430
HFEBN52	82	810429	AL359399	699	1-430
HAJBH69	99	812164	AL035496	700	1-565 855-1099 2067-4150 4159-4449 4474-4747 5104-5234 5852-5937 6421-6561 7510-7799 8583-9223 9477-9989 10109-10208 11605-12056 12474-12574 13276-13359 14559-14890 14968-16129 16629-16740 16984-17214 17460-17816
HMAER78	102	702735	AC074333	701	1-357
HTEPM33	105	870561	AL132776	702	1-42 1020-1195 2173-2338 6839-7029 11880-12103
HTEPM33	105	870561	AL132776	703	1-173
HTEPM33	105	870561	AL132776	704	1-791
HDTEJ81	107	919873	AC004707	705	1-74

					285-478 553-872 2612-4708 4745-5348
HDTEJ81	107	919873	AC004707	706	1-318 1694-1796 2541-2601 2726-3334 4150-4509 4632-4791 5026-5134 8019-8346 8944-9470 12238-12412 14290-16770 17028-17771 19503-19606 21647-22467
HCGMG56	118	953660	AC004707	707	1-604 641-2737 4477-4796 4871-5064 5275-5348
HCGMG56	118	953660	AC004707	708	1-821 2862-2965 4697-5440 5698-8178 10056-10230 12998-13524 14122-14449 17334-17442 17677-17836 17959-18318 19134-19742 19867-19927 20672-20774 22150-22467
HE8MI76	123	911474	AL137008	709	1-97 446-576 761-1233 3775-3946

					4867-5024 5520-5729 8345-8467 10681-10858 11553-11879 12483-14416 14439-14940 15077-15549 15779-15907 20468-20613 21617-21807 23498-23598 23636-23733 23851-24271 25734-26340 26686-26850 27674-27830 28001-28075 29807-30301 30480-31201 31218-31488 31758-31878 32812-33412 33772-34391 34798-34911 36778-37158 37234-37825 38688-39969
HNSAB28	154	881286	AC010188	710	1-151 1103-1517 2286-2664 4067-4735 4740-4859 5876-6449 7178-7278 7318-7451 7539-7983 8131-8235 8418-9210 9619-9776 11087-12216

HNSAB28	154	881286	AC010188	711	1-420 442-1482
HTTEP70	155	917729	AC005546	712	1-84 94-607 687-742 971-1123 1271-1463 2970-3130 3726-3851 3920-4035 4307-4724 5193-5352 6432-6975 7007-7190 7271-7363 7504-7738 7747-7841 8468-8620 8879-8995 9088-9166 9632-9736 9743-9875 9953-10058 10840-10955 11128-11473 11656-11837
HTTEP70	155	917729	AC005546	713	1-74
HUSGZ51	162	955542	AC018568	714	1-1718
HUSGZ51	162	955542	AC018568	715	1-425
HNFFR23	165	585289	AC008751	716	1-343
HFOZC96	167	926685	AF238376	717	1-145 304-383 2385-2851 3341-3588 4343-4428 4631-4797 6602-6724 7496-8173 8368-9341
HHERB37	169	708477	AL355377	718	1-505 662-2071

HKAED89	178	827573	AF038458	719	1-630 1311-1416 2481-4022 4952-5252 6370-6479 7623-8269
HWWGT02	185	908017	AC004188	720	1-150 500-1073 1818-2402 2467-3243 3940-4026
HWWGT02	185	908017	AB014086	721	1-150 500-1072 1817-2401 2466-3242 3939-4025
HWWGT02	185	908017	AC004188	722	1-699
HWWGT02	185	908017	AB014086	723	1-699
HODFI03	187	918008	AC007041	724	1-402 3126-3268 3901-4312 4472-5358 6517-6670 6767-7912 8251-8380 8609-8730 9249-9427 9575-10072 10942-11345 11359-11545 11877-14991
HODFI03	187	918008	AC007041	725	1-322
HODFI03	187	918008	AC007041	726	1-381
HWHHR02	188	919169	AF053356	727	1-71 234-304 320-826 878-1099 1233-1683 2077-3297
HWHHR02	188	919169	AF053356	728	1-434
HWHHR02	188	919169	AF053356	729	1-152

HSVBQ03	189	924850	AC004477	730	1-326 1029-1626 2309-2345 2958-3015 3982-4124 5005-5248 5482-6071 6519-6577 7045-7136 7692-7780 8037-8184 9575-9866 10372-10789 11501-11618
HE9GZ52	192	964579	AL359881	731	1-183 574-652 897-1212 1599-1902
HE9GZ52	192	964579	Z98884	732	1-569 4314-4514 4905-4983 5228-5543 5930-6233
HE9GZ52	192	964579	Z98884	733	1-298
HSDJH63	195	941120	AC012224	734	1-1316
HSDJH63	195	941120	AC044892	735	1-1394
HSDJH63	195	941120	AC006252	736	1-1394
HSDJH63	195	941120	AC006252	737	1-111 281-410 1326-1983
HWDAE40	199	947007	AC016605	738	1-2114
HWDAE40	199	947007	AC008917	739	1-107 510-2620
HWDAE40	199	947007	AC008917	740	1-426
HUVHH77	200	948377	AL132641	741	1-2545
HUVHH77	200	948377	AL132641	742	1-4063 4990-5958
HUVHH77	200	948377	AL132641	743	1-775
HTLIT03	201	966870	AC009077	744	1-89 471-679 809-978

					3619-4024 5223-5374 6500-6876 7519-7607 8279-8386 8536-9192
HTLIT03	201	966870	AC004531	745	1-84 643-971 1003-1047 2794-2855 7497-7541 8459-8546 8885-9170 12745-12811 12995-13065 14987-15122 16524-16612 16994-17202 17332-17501 20142-20547 21746-21897 23023-23399 24802-24909 25059-25715
HTLIT03	201	966870	AC009077	746	1-139
HTLIT03	201	966870	AC009077	747	1-114
HTLIT03	201	966870	AC004531	748	1-108
HRABP94	209	970481	AL136222	749	1-73 226-264 289-1812 1968-2177 2300-2813 2951-3091 3146-3222 3597-3888
HRABP94	209	970481	AL109947	750	1-35 90-146 603-976 1504-1816 1908-2118 2389-2496

					3139-4163 5195-5455 5670-5784 5971-6356 6875-7024 7362-8082 8097-9620 9776-9985 10108-10621 10759-10899 10954-11030 11405-11696
HRABP94	209	970481	AL359711	751	1-35 90-146 603-976 1504-1816 1908-2118 2389-2496 3139-4163 5195-5455 5670-5784 5971-6356 6875-7024 7362-8082 8097-9620 9776-9985 10108-10621 10759-10899 10954-11030 11405-11696
HRABP94	209	970481	AL136222	752	1-479 502-655 841-948 1038-1393 1624-1713 1856-1951 2057-2373 2467-2567 2696-3160
HRABP94	209	970481	AL109947	753	1-479 502-655

					841-948 1038-1393 1624-1713 1856-1951 2057-2373 2467-2567 2696-3160
HRABP94	209	970481	AL359711	754	1-479 502-655 841-948 1038-1393 1624-1713 1856-1951 2057-2373 2467-2567 2696-3160
HRABP94	209	970481	AL109947	755	1-532
HRABP94	209	970481	AL359711	756	1-532
HTTHF21	213	921596	AC013264	757	1-1071 3263-3406 4512-4719
HTTHF21	213	921596	AC074092	758	1-1071
HTTHF21	213	921596	AC013264	759	1-527
HTTHF21	213	921596	AC074092	760	1-527
HJMBN52	215	966226	AF276758	761	1-184 756-1081 1289-1644 3033-3467
HJMBN52	215	966226	AC024049	762	1-184 755-1080 1283-1637 3026-3458
HSIGQ50	233	932448	AC015551	763	1-250 418-479 572-642 1076-1152 2851-2927 3010-3133 3242-3338 3438-3518 3612-3715

					3840-3987 4189-4308 4594-4869 4912-5046 5149-5298 5473-6592 6692-6760 6805-7073 7286-7514 7744-7833 8003-8545 8778-8913 9249-9703
HSIGQ50	233	932448	AC019214	764	1-160 713-910 1069-1269 3997-4098 4303-4397 5035-5098 5740-5796 6024-6155 6697-6813 6937-7029 7110-7349 7432-7571 7573-7601 7834-7907 8326-8490 8712-8804 8894-8979 9090-9171 9368-9467 9622-9730 9821-10012 10197-10277 10440-10562 10668-11103 11203-11432 11937-12052 12251-12312 12794-13183

					13257-13343 13483-13996 14001-14146 14369-14483 14587-15046 15053-15302 15470-15534 15624-15695 16128-16212 17904-17980 18066-18189 18298-18394 18494-18574 18668-18771 18896-19043 19245-19364 19650-19925 19968-20102 20205-20354 20529-21648 21748-21816 21861-22129 22341-22569 22799-22888 23058-23600 23833-23968 24304-24757
HSIGQ50	233	932448	AC019214	765	1-803 1028-1918
HNSMB24	235	971537	AC015555	766	1-61 464-586 752-1423 3455-3587 5766-5958 6757-7115 8075-8329 8778-8876 12309-12455 13123-13279 16212-17107
HNSMB24	235	971537	AP001623	767	1-61

					464-586 752-1423 3455-3580 4976-5021 5793-5958 6757-7115 8075-8329 8778-8876 12305-12451 13119-13275 16208-17104
HNSMB24	235	971537	AC015555	768	1-674
HNSMB24	235	971537	AP001623	769	1-674

[43] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HFRBN59	1106393	11	blastx.14	Hypothetical fimbrial chaperone in pepN-pyrD intergenic region . [Escherichia coli]	gi|4062512|dbj|BAA35699.1|	82%	212	445
HFRBN59	739539	237	HMMER 1.8	PFAM: Fimbrial proteins	PF00419	19.62	86	232
HE2KJ64	906019	12	HMMER 1.8	PFAM: SCP-like extracellular Proteins	PF00188	66.3	35	277
			blastx.14	(AF109674) late gestation lung protein 1 [Rattus norvegicus]	gi|4324682|gb|AAD16986.1|	74%	2	364
HAGDV32	1178626	13	blastx.2	Diacylglycerol kinase iota (Fragment).	sp|AAF43006|AAF43006	100%	19	243
HAGDV32	699372	238	HMMER 1.8	PFAM: Ank repeat	PF00023	15.79	41	121
HLICC37	856958	14	HMMER 2.1.1	PFAM: Ank repeat	PF00023	33.1	53	151
HBGBU96	1121900	15	blastx.2	hypothetical 30.8 kD protein in gltF-nanT intergenic region - Escherichia coli (strain K-12)	pir|H65113|H65113	79%	3	449
HBGBU96	848220	239	HMMER 2.1.1	PFAM: ROK family	PF00480	65.2	3	125
HAJCQ63	823850	16	HMMER 2.1.1	PFAM: Ank repeat	PF00023	96.9	175	267

HLMMV66	1153903	17	blastx.2	CENTAURIN BETA2.	sp|Q9UQR3|Q9UQR3	63%	242	628
HLMMV66	926188	240	HMMER 1.8	PFAM: Ank repeat	PF00023	17.86	245	322
			blastx.14	similar to HUMORFU (D26069) [Homo sapiens]	gi|488505|dbj|BAA06418.1|	62% 81% 86% 71% 39% 43%	230 337 404 378 173 99	382 384 448 419 256 146
HLWAR08	1096389	18	blastx.14	(AF160798) calcium transporter CaT1 [Rattus norvegicus]	gi|5712756|gb|AAD47636.1|AF160798_1	91% 100% 89% 30% 46%	151 1 447 1 61	450 144 533 99 99
HLWAR08	959139	241	HMMER 1.8	PFAM: Ank repeat	PF00023	13.97	3	44
HBGTT76	1152327	19	blastx.2	Shank3b protein.	sp|CAB89816|CAB89816	72%	7	468
HBGTT76	903653	242	HMMER 2.1.1	PFAM: Ank repeat	PF00023	62.3	197	295
			blastx.14	(AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]	gi|5262748|emb|CAB45688.1|	72% 47%	131 499	556 561
HMCFO24	924647	20	HMMER 2.1.1	PFAM: Ank repeat	PF00023	59.5	216	308
			blastx.14	UNC-44 [Caenorhabditis elegans]	gi|790608|gb|AAA85854.1|	41% 34% 37% 36% 48% 43%	186 57 195 174 219 192	323 203 353 323 323 323

HBIOM94	973137	21	HMMER 2.1.1	PFAM: Ank repeat	PF00023	34%	174		323
			blastx.2	contains 10 ankyrin-like repeats; similar to human ankyrin, 1 bursaria Chlorella virus 1]	gb|AAC96986.1|	48%	102		182
						46%	90		173
						38%	60		167
						33%	75		182
						42%	219		323
						26%	78		200
						29%	78		170
						47%	3		71
						34%	3		71
						47%	9		65
						50%	427		462
HBJLR11	1012465	22	blastx.2	Sterol regulatory element binding protein 3.	sp|AAF67491|AAF67491	58%	62	37.4	388
HBJLR11	956568	243	HMMER 1.8	PFAM: LIM domain containing proteins	PF00412	53.39	2088	476	574
			blastx.14	mutant sterol regulatory element binding protein-2 1	gi|841318|gb|AAA85718.1|	66%	2097		1804
						45%	1728		1585
						66%	531		478
HBJLR11	975276	244	blastx.14	mutant sterol regulatory element binding protein-2 1	gi|841318|gb|AAA85718.1|	63%	1037		762
						60%	1085		1041
HLTER04	590990	23	HMMER 2.1.1	PFAM: DnaJ central domain (4 repeats)	PF00684	128.3	90	191	350
HMSMU30	823859	245	HMMER 1.8	PFAM: Ank repeat	PF00023	12.82	191		244

H2MBY83	752124	25	HMMER 2.1.1	PFAM: Protein of unknown function	PF01951	137	80	493
			blastx.2	CG6353 PROTEIN.	sp|Q9VD92|Q9VD92	58%	80	493
HBUAH93	1164739	26	blastx.2	CDNA FLJ10852 FIS, CLONE NT2RP4001498, WEAKLY SIMILAR TO 1	sp|BAA91856|BAA91856	51%	130	1299
HBUAH93	810424	246	HMMER 2.1.1	PFAM: Ank repeat	PF00023	35.4	340	438
HMZAD58	975304	27	HMMER 2.1.1	PFAM: Putative GTP-ase activating protein for Arf	PF01412	196.5	362	739
			blastx.14	(AF124491) ARF GTPase-activating protein GIT2 [Homo sapiens]	gi|4691728|gb|AAD28047.1|AF124491_1	89% 100% 97% 25% 34% 33% 29%	368 1964 1712 1730 2000 1280 1445	1813 2509 1972 1894 2104 1360 1546
HCHNH17	975378	28	HMMER 2.1.1	PFAM: LIM domain containing proteins	PF00412	31.3	896	1009
			blastx.2	LIM and cysteine-rich domains protein 1.	sp|AAF34411|AAF34411	90% 34%	116 917	1009 1021
HBWAJ55	971772	247	HMMER 2.1.1	PFAM: Ank repeat	PF00023	321.4	820	918
			blastx.2	ankyrin G [Homo sapiens]	gb|AAA64834.1|	95% 39% 37% 34% 36% 32% 33% 39%	91 163 130 163 166 106 103 163	1239 1182 1182 1206 1185 1182 1188 609

						38%	148	597
HNJCE31	1152346	30	blastx.2	ASB-1 PROTEIN.	sp|Q9Y576|Q9Y576	100%	1230	244
HNJCE31	911597	248	HMMER 2.1.1	PFAM: Ank repeat	PF00023	85	354	440
			blastx.14	(AF156777) ASB-1 protein [Homo sapiens]	gi|5306062|gb|AAD41894.1|AF156777_1 .	100% 100% 26%	81 34 985	1031 75 1074
HKAIU14	919538	31	HMMER 2.1.1	PFAM: Uncharacterised protein family	PF01980	147.9	148	519
			blastx.2	CDNA FLJ20206 FIS, CLONE COLF1582.	sp|BAA91013|BAA91013	99%	25	1314
HCE4I12	911586	32	HMMER 2.1.1	PFAM: Ank repeat	PF00023	72.3	106	195
			blastx.2	CG6268 PROTEIN.	sp|Q9VCA7|Q9VCA7	70% 48% 44% 44% 39% 36% 35% 34% 57% 53%	1 13 28 4 4 4 4 4 315 315	369 396 312 288 312 291 312 279 356 359
HFOYI18	926488	33	HMMER 2.1.1	PFAM: Domain of unknown function	PF01942	26.4	255	569
			blastx.14	(AC004077) hypothetical protein [Arabidopsis thaliana]	gi|3128208|gb|AAC26688.1|	23% 32% 46% 58%	426 144 300 726	716 308 422 797
HHEDM89	945055	34	HMMER 2.1.1	PFAM: N2,N2-dimethylguanosine tRNA methyltransferase	PF02005	132	22	828

			blastx.2	(AP000007) 381aa long hypothetical N2,N2-dimethylguanosine tRNA methyltransferase [Pyrococcus horikoshii]	dbj|BAA30948.1|	35%	16	720
HFXKW18	945288	35	HMMER 2.1.1	PFAM: Domain of unknown function 2	PF00563	65.2	2104	2310
			blastx.2	Hypothetical 67.7 kd protein CY02B10.18C. [Escherichia coli]	dbj|BAA35528.1|	99%	529	2337
HBIMF04	951601	36	HMMER 2.1.1	PFAM: TraB family	PF01963	191.2	336	1043
			blastx.2	(AL022328) dJ402G11.4 (novel protein similar to C. elegans F38A5.2 (isoform 1)) [Homo sapiens]	emb|CAB63043.1|	99% 80% 100%	405 1085 160	1130 1249 237
HEEAU28	946972	249	HMMER 2.1.1	PFAM: LIM domain containing proteins	PF00412	67.2	46	207
			blastx.14	ajuba; jub [Mus musculus]	gi|1710382|gb|AAB38287.1|	67% 37%	13 292	327 339
HDPKI66	823854	38	HMMER 2.1.1	PFAM: Ank repeat	PF00023	50.4	293	391
			blastx.2	DIFFERENTIATION ENHANCING FACTOR 1.	sp|O97902|O97902	62%	2	1399
HOCQD08	972981	39	HMMER 2.1.1	PFAM: Protein of unknown function	PF02000	42.2	38	307
			blastx.14	phosphorylation regulatory protein HP-10 - human	pir|A61382|A61382	78% 98%	320 78	715 326

HDPRP54	1228283	40	blastx.2	CDNA FLJ10852 FIS, CLONE NT2RP4001498, WEAKLY SIMILAR TO 1	sp|BAA91856|BAA91856	96%	75	1517
HDPRP54	502892	250	HMMER 1.8	PFAM: Ank repeat	PF00023	20.99	330	401
HE2BW32	609468	41	HMMER 2.1.1	PFAM: MSP (Major sperm protein) domain	PF00635	87.1	19	192
HAJAU21	670606	42	HMMER 2.1.1	PFAM: Adaptin N terminal region	PF01602	194.1	2	322
			blastx.2	gamma-adaptin precursor - mouse	pir|A36680|A36680	95%	2	319
HE8DL23	693641	43	HMMER 2.1.1	PFAM: Adaptin N terminal region	PF01602	131.4	29	343
			blastx.2	GAMMA2-ADAPTIN.	sp|O75504|O75504	83% 100%	29 408	406 470
HFTCM92	928851	44	HMMER 1.8	PFAM: LIM domain containing proteins	PF00412	43.25	178	351
			blastx.2	ALPHA-ACTININ-2 ASSOCIATED LIM PROTEIN.	sp|O70209|O70209	36% 90%	22 22	357 51
HFTCM92	948605	251	blastx.14	carboxyl terminal LIM domain protein [Homo sapiens]	gi|1905874|gb|AAC05580.1|	64% 30%	581 662	456 585
HE6BQ76	775616	45	HMMER 2.1.1	PFAM: Double-stranded RNA binding motif	PF00035	28.1	155	223
			blastx.2	PROTEIN ACTIVATOR OF THE INTERFERON-INDUCED PROTEIN KINASE.	sp|O75569|O75569	66% 94%	146 109	340 159
HAMFP60	715097	46	HMMER	PFAM: Clathrin adaptor	PF01217	150.3	164	460

			2.1.1	complex small chain				
HHFHY84	715098	47	HMMER 2.1.1	PFAM: Clathrin adaptor complex small chain	PF01217	78.2	129	305
HE6FD03	1150900	48	blastx.2	CG1800 PROTEIN.	sp|Q9V9V7|Q9V9V7	36%	846	403
HE6FD03	859840	252	HMMER 2.1.1	PFAM: Double-stranded RNA binding motif	PF00035	26.1	283	390
HDTFT90	1165338	49	blastx.2	CDNA FLJ10860 FIS, CLONE NT2RP4001568, WEAKLY SIMILAR TO 1	sp|BAA91862|BAA91862	88% 66%	2 211	217 399
HDTFT90	944518	253	HMMER 1.8	PFAM: Ank repeat	PF00023	17.29	190	249
HPJCU63	904598	254	HMMER 2.1.1	PFAM: Ank repeat	PF00023	187.9	735	833
			blastx.14	ankyrin [Drosophila melanogaster]	gi|557084|gb|AAC37208.1|	33% 32% 30% 31% 36% 30% 37% 29% 36% 25% 38% 36% 31% 32% 41% 29% 32% 42%	126 126 123 123 339 111 219 129 201 204 144 120 123 342 135 117 501 744	833 815 725 638 737 707 605 710 593 731 503 413 521 707 404 410 695 827

						40% 37% 32% 28% 35% 56% 34%	726 738 600 732 732 923 726	815 833 737 836 824 970 812
HFITE38	793203	51	HMMER 2.1.1	PFAM: MAGE family	PF01454	47.4	176	349
			blastx.2	DJ14O9.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE).	sp|O76058|O76058	92% 85%	89 14	352 136
HDPDH64	796509	52	HMMER 2.1.1	PFAM: Adaptin N terminal region	PF01602	46.4	148	246
HFKKS58	1158800	53	blastx.2	CDNA FLJ10259 FIS, CLONE HEMBB1000947, HIGHLY SIMILAR TO 1	sp|BAA91511|BAA91511	99%	2	1135
HFKKS58	914398	255	HMMER 2.1.1	PFAM: RNase3 domain.	PF00636	102.6	443	712
HE8CM38	1197903	54	blastx.2	NG28.	sp|Q9Z1P7|Q9Z1P7	61%	2	565
HE8CM38	932013	256	HMMER 2.1.1	PFAM: Ank repeat	PF00023	93.8	257	355
			blastx.14	similar to ankyrin of Chromatium vinosum. [Homo sapiens]	gi|1136404|dbj|BAA11489.1|	99% 90%	2 525	508 557
HAJBU67	856922	55	HMMER 2.1.1	PFAM: eRF1-like proteins	PF01605	28.1	514	606
HHEHD10	1204696	56	blastx.2	hypothetical protein DKFZp434B1517.1 -	pir|T34532|T34532	82% 96%	562 3	1458 278

				human (fragment)				
HHEHD10	894411	257	HMMER 1.8	PFAM: LIM domain containing proteins	PF00412	28.72	48	224
HHEND45	919630	57	HMMER 1.8	PFAM: Double-stranded RNA binding motif	PF00035	12.86	25	114
HE8EQ22	1031960	58	blastx.2	ASB-3 PROTEIN (CDNA FLJ10123 FIS, CLONE HEMBA1002939, WEAKLY 1	sp|Q9Y575|Q9Y575	82% 94% 42%	199 695 674	702 751 751
HE8EQ22	911594	258	HMMER 2.1.1	PFAM: Ank repeat	PF00023	128.9	430	528
			blastx.14	(AF156778) ASB-3 protein [Homo sapiens]	gi|5306064|gb|AAD41895.1|AF156778_1	94% 37% 70% 36%	199 433 792 718	786 615 884 783
HSACD83	911588	59	HMMER 2.1.1	PFAM: Ank repeat	PF00023	47	160	258
			blastx.2	WUGSC:H_DJ1035O02.1 PROTEIN (FRAGMENT).	sp|Q9UDM3|Q9UDM3	58% 53%	169 438	402 554
HHGBO53	1091714	60	blastx.2	hypothetical protein DKFZp434B1517.1 - human (fragment)	pir|T34532|T34532	92% 93% 51% 25%	235 685 27 611	402 771 128 769
HHGBO53	894375	259	HMMER 1.8	PFAM: LIM domain containing proteins	PF00412	26.8	133	252
HE8FD82	1154785	61	blastx.2	Hypothetical 35.8 kDa protein.	sp|CAC09448|CAC09448	99%	8	811
HE8FD82	909634	260	HMMER 2.1.1	PFAM: Putative GTP-ase activating protein for Arf	PF01412	184.7	256	618
			blastx.14	(AL031633) similar to	gi|3880859|emb|CAA	57%	265	510

				Ank repeat (2 domains); cDNA 1	21032.1|	42% 46% 46%	502 733 128	732 861 172
HOHAS44	914810	62	HMMER 2.1.1	PFAM: 7-fold repeat in Clathrin and VPS	PF00637	104.3	2	379
			blastx.14	clathrin heavy chain [Bos taurus]	gi|969024|gb|AAC48524.1|	100%	2	664
HE8OF42	1117857	63	blastx.2	CDNA FLJ20636 FIS, CLONE KAT03434.	sp|BAA91302|BAA91302	58% 36% 35% 57%	199 208 181 488	486 483 489 544
HE8OF42	810432	261	HMMER 2.1.1	PFAM: Ank repeat	PF00023	47.6	298	396
HSKHS71	1154798	64	blastx.2	ankyrin repeat protein A682L - Chlorella virus PBCV-1	pir|T18184|T18184	40% 33% 35% 32% 31% 34% 27%	52 52 4 7 7 7 4	477 726 504 486 504 405 456
HSKHS71	911592	262	HMMER 2.1.1	PFAM: Ank repeat	PF00023	63.1	94	192
			blastx.14	contains 10 ankyrin-like repeats; similar to human 1 [Paramecium bursaria Chlorella virus 1]	gi|2447128|gb|AAC96986.1|	42% 36% 35% 35% 38% 31% 40% 35%	106 97 103 100 103 103 196 1	366 357 372 372 357 366 381 84
HISBT75	1181020	65	blastx.2	LIM DOMAIN PROTEIN CLP-36.	sp|O00151|CL36_HUMAN	40%	37	360

HISBT75	963281	263	HMMER 1.8	PFAM: LIM domain containing proteins	PF00412	43.09	129	302
			blastx.14	carboxyl terminal LIM domain protein [Homo sapiens]	gi|1905874|gb|AAC05580.1|	64% 25%	183 12	308 179
HFVKF77	930964	66	HMMER 2.1.1	PFAM: 7-fold repeat in Clathrin and VPS	PF00637	642.4	3205	2780
			blastx.14	clathrin heavy chain [Bos taurus]	gi|969024|gb|AAC48524.1|	98% 100% 100% 36% 39% 46% 48% 57% 30% 46% 28%	3718 1741 3788 2014 3788 1936 3535 3289 3196 3558 2011	1748 1583 3705 1940 3720 1892 3461 3248 3128 3514 1937
HJABW64	931402	67	HMMER 2.1.1	PFAM: Leucine Rich Repeat	PF00560	30.1	340	408
			blastx.2	hypothetical protein [Silene latifolia]	emb|CAA73132.1|	48% 39%	115 115	456 456
HCEMY90	932927	68	HMMER 2.1.1	PFAM: PWWP domain	PF00855	48.7	67	234
			blastx.2	WHSC1 PROTEIN.	sp|O96028|O96028	62% 65%	67 546	585 605
HHFLF63	933854	69	HMMER 2.1.1	PFAM: Repeat in ubiquitin-activating (UBA) proteins	PF02134	110.2	487	654
			blastx.14	Sbx [Mus musculus]	gi|54058|emb|CAA44465.1|	36% 44% 35%	4 421 277	285 654 336

						41% 58%	642 707	713 742
HSKAN19	935229	70	HMMER 2.1.1	PFAM: Leucine Rich Repeat	PF00560	69.4	757	825
			blastx.14	similar to yeast adenylate cyclase (S56776) [Homo sapiens]	gi|1504042|dbj|BAA13220.1|	51%	1	1176
HE9SE88	894905	264	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052	1.3	115	189
HDTDG41	942490	72	HMMER 2.1.1	PFAM: Leucine Rich Repeat	PF00560	33.6	236	307
			blastx.14	proteoglycan I precursor [Homo sapiens]	gi|306884|gb|AAA36009.1|	60% 63% 34% 36% 32%	206 111 120 84 114	574 224 206 158 206
HTEPX32	870698	73	HMMER 1.8	PFAM: Double-stranded RNA binding motif	PF00035	36	508	699
			blastx.2	testis nuclear RNA binding protein - mouse	pir|I48840|I48840	87% 80% 67%	190 716 1179	699 1207 1325
HEGAB84	1128320	74	blastx.2	ankyrin-related protein unc-44 - Caenorhabditis elegans (fragment)	pir|A57282|A57282	34% 31% 38%	71 119 197	475 475 469
HEGAB84	823900	265	HMMER 2.1.1	PFAM: Ank repeat	PF00023	36.9	205	315
			blastx.2	ankyrin 3 [Mus musculus]	gb|AAB01605.1|	37%	28	348
HTEKQ12	1213746	75	blastx.2	probable ATPase SKD3 [imported] - mouse	pir|I49045|I49045	83% 84%	256 112	1869 393
HTEKQ12	947964	266	HMMER 2.1.1	PFAM: Ank repeat	PF00023	52	140	238